

Jarrell, Noble

10190146

From: Ramirez, Delia
Sent: Tuesday, May 16, 2006 11:22 AM
To: Jarrell, Noble
Subject: 10/689,576

Hi,

I would like to request the following searches:

1. SEQ ID NO:3 in the protein databases (commercial & interference)
2. an alignment of SEQ ID NO: 1, 3, 4 and 5

Thank you very much,

Delia M. Ramirez, Ph.D.
Patent Examiner
Recombinant Enzymes-Art Unit 1652
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Alexandria, VA 22314
(571) 272-0938
delia.ramirez@uspto.gov

5-17-06

Noble
J 5118706
Compugen GC
IC
265AA
SONZ
SPR

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GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 16, 2006, 13:24:09 ; Search time 38 Seconds
(without alignments)
40.512 Million cell updates/sec

Title: US-10-689-576-3

Perfect score: 79

Sequence: 1 ANSFVGTAAQVYSPPELL 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Listing first 45 summaries

1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	67	84.8	766	2	hypothetical prote
2	67	84.8	1081	2	probable protein k
3	66	83.5	898	2	hypothetical prote
4	64	81.0	550	2	phosphoinositide-d
5	63	79.7	592	2	probable protein k
6	61	77.2	404	2	hypothetical prote
7	60	75.9	372	2	hypothetical prote
8	60	75.9	393	1	mitogen-activated
9	60	75.9	393	1	mitogen-activated
10	60	75.9	393	1	mitogen-activated
11	60	75.9	393	1	mitogen-activated
12	60	75.9	393	1	mitogen-activated
13	60	75.9	393	1	mitogen-activated
14	60	75.9	395	1	mitogen-activated
15	60	75.9	397	1	mitogen-activated
16	60	75.9	400	1	mitogen-activated
17	60	75.9	401	1	mitogen-activated
18	60	75.9	428	1	mitogen-activated
19	60	75.9	432	1	mitogen-activated
20	60	75.9	572	2	mitogen-activated
21	60	75.9	911	2	mitogen-activated
22	60	75.9	915	2	mitogen-activated
23	60	75.9	923	2	mitogen-activated
24	60	75.9	927	2	mitogen-activated
25	60	75.9	966	2	mitogen-activated
26	60	75.9	1465	2	mitogen-activated
27	59	72.4	2	2	mitogen-activated
28	58	73.4	526	2	mitogen-activated
29	58	73.4	566	2	mitogen-activated

30	58	73.4	893	2	mitogen-activated
31	57	72.2	312	2	mitogen-activated
32	57	72.2	312	2	mitogen-activated
33	57	72.2	387	1	mitogen-activated
34	57	72.2	400	1	mitogen-activated
35	57	72.2	926	2	mitogen-activated
36	57	72.2	934	2	mitogen-activated
37	57	72.2	949	2	mitogen-activated
38	56	70.9	354	2	mitogen-activated
39	56	70.9	726	2	mitogen-activated
40	55	69.6	320	2	mitogen-activated
41	55	69.6	785	2	mitogen-activated
42	54	68.4	245	2	mitogen-activated
43	54	68.4	357	2	mitogen-activated
44	54	68.4	363	2	mitogen-activated
45	54	68.4	363	2	mitogen-activated

ALIGNMENTS

RESULT 1
S69657
hypothetical protein YDR490C - Yeast (Saccharomyces cerevisiae)
C:Species: Saccharomyces cerevisiae
C>Date: 22-Aug-1996 #sequence_revision 06-Sep-1996 #text_change 05-Oct-2004
C:Accession: S69657
R:Dieckrich, F.S.
Submitted to the EMBL Data Library, August 1995
A:Description: The sequence of S. cerevisiae cosmid 9410, 8035, 8166, and 9787.
A:Reference number: S69554
A:Accession: S69657
A:Molecule type: DNA
A:Residues: 1-766 <DIE>
A:Cross-references: UNIPROT:Q03407, UNIPARC:UPI000006A3C7, EMBL:U33050, NID:g927726; PID
C:Genetics:
A:Gene: SGD:PKH1
A:Cross-references: SGD:S0002898
A:Map position: 4R
C:Keywords: ATP
F:123-391/Domain: protein kinase homology <KIN>
F:131-139/Region: protein kinase ATP-binding motif

Query Match 84.8%; Score 67; DB 2; Length 766;
Best Local Similarity 81.2%; Pred. No. 0.0016;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ANSFVGTAAQVYSPPELL 16
DB 294 SKSFVGTAAQVYSPPELL 309

RESULT 2
S51899
probable protein kinase HRC1081 (EC 2.7.1.-) - Yeast (Saccharomyces cerevisiae)
N:Alternate names: protein O0784; protein YOL100W
C:Species: Saccharomyces cerevisiae
C>Date: 05-May-1995 #sequence_revision 03-Aug-1995 #text_change 05-Oct-2004
C:Accession: S51899; S59175; S66796
R:Vanderbol, M.; Durand, P.; Portetelle, D.; Hilger, F.
Submitted to the EMBL Data Library, January 1995
A:Description: Sequence analysis of a 44kb DNA fragment of yeast chromosome XV including
and a Delta.
A:Reference number: S51848
A:Accession: S51899
A:Molecule type: DNA
A:Residues: 1-1081 <VAN>
A:Cross-references: UNIPROT:Q12236, UNIPARC:UPI000004F9FC, EMBL:Z48149, NID:g663234; PID
R:Vanderbol, M.; Durand, P.; Portetelle, D.; Hilger, F.
Yeast 11, 1069-1075, 1995
A:Title: Sequence analysis of a 44 kb DNA fragment of yeast chromosome XV including the
a delta element.
A:Reference number: S59156; MUID:96076631; PMID:7502582

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A/Accession: S59175
A/Status: nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-1081 <YAM>
A/Cross-references: UNIPARC:UPI000004F9FC; EMBL:Z48149; NID:g663234; PIDN:CAA88162.1; PT
A/Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1995
R/Durand, P.; Hilger, F.; Portecelle, D.; Vanderbol, M.
submitted to the Protein Sequence Database, July 1996
A/Reference number: S66791
A/Accession: S66796
A/Molecule type: DNA
A/Residues: 1-1081 <DUR>
A/Cross-references: UNIPARC:UPI000004F9FC; EMBL:Z74842; NID:g1419951; PIDN:CAA99113.1; F
A/Experimental source: strain S286C
C/Genetics:
A/Gene: SGD:PKH2
A/Cross-references: SGD:S0005460
A/Map position: 15L
C/Keywords: ATP; phosphotransferase
F:17-443/Domain: protein kinase homology <KIN>
F:185-193/Region: protein kinase ATP-binding motif

Query Match      84.8%; Score 67; DB 2; Length 1081;
Best Local Similarity 81.2%; Pred. No. 0.0023;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 ANSFVGTAGYVSPELL 16
Db      346 SKSFVGTAEVYVSPELL 361
: |||||:|||||

RESULT 3
S69634
hypothetical protein YDR466v - yeast (Saccharomyces cerevisiae)
C/Species: Saccharomyces cerevisiae
C/Date: 22-Aug-1996 #sequence_revision 06-Sep-1996 #text_change 05-Oct-2004
C/Accession: S69634
R/Dietrich, F.S.
submitted to the EMBL Data Library, August 1995
A/Description: The sequence of S. cerevisiae cosmid 9410, 8035, 8166, and 9787.
A/Reference number: S69554
A/Accession: S69634
A/Molecule type: DNA
A/Residues: 1-898 <DIE>
A/Cross-references: UNIPROT:Q03306; UNIPARC:UPI000006C12E; EMBL:U33050; NID:g927726; PIT
A/Genetics:
A/Cross-references: SGD:S0002874
A/Map position: 4R
C/Keywords: ATP
F:9-293/Domain: protein kinase homology <KIN>
F:17-25/Region: protein kinase ATP-binding motif

Query Match      83.5%; Score 66; DB 2; Length 898;
Best Local Similarity 92.9%; Pred. No. 0.0028;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      3 SFFVGTAGYVSPELL 16
Db      189 SFFVGTAEVYVSPELL 202
: |||||:|||||

RESULT 4
T40486
phosphoinositide-dependent protein kinase 1 (EC 2.7.1.-) SPBC4C3.11 [imported] - fission
C/Species: Schizosaccharomyces pombe
C/Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 09-Jul-2004
R/Wood, V.; Rajadream, M.A.; Barrell, B.G.; Lauber, J.; Hilbert, H.; Duessenhoef, A.
submitted to the EMBL Data Library, February 1998
A/Reference number: Z21910
A/Accession: T40486
A/Status: preliminary
A/Molecule type: DNA

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A/Residues: 1-420 <WOO>
A/Cross-references: UNIPROT:Q9Y7J6; UNIPARC:UPI0000069850; EMBL:AL021730; PIDN:CAA16833.1
R/Oliver, K.; Harris, D.; Wood, V.; Rajadream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, March 1998
A/Reference number: Z21869
A/Accession: T39692
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 385-550 <OLI>
A/Cross-references: UNIPARC:UPI000006A777; EMBL:AL049489; PIDN:CA839805.1; GSPDB:GN00067
A/Experimental source: strain 972h-; cosmid c1778
C/Genetics:
A/Gene: SPBC4C3.11; SPDB:SPBC1778.10C
A/Map position: 2
C/Keywords: phosphotransferase

Query Match      81.0%; Score 64; DB 2; Length 550;
Best Local Similarity 80.0%; Pred. No. 0.0036;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      2 NSFVGTAGYVSPELL 16
Db      218 SSFVGTAEVVAPELL 232
: |||||:|||||

RESULT 5
T43402
probable protein kinase (EC 2.7.1.-) - fission yeast (Schizosaccharomyces pombe)
C/Species: Schizosaccharomyces pombe
C/Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
C/Accession: T43402; T41425
R/Niederberger, C.
submitted to the EMBL Data Library, July 1998
A/Reference number: Z22486
A/Accession: T43402
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-592 <NIE>
A/Cross-references: UNIPROT:Q12701; UNIPARC:UPI0000069B00; EMBL:X92880; PIDN:CAA67672.1
A/Experimental source: strain h90
R/Wood, V.; Rajadream, M.A.; Barrell, B.G.; Murphy, L.; Harris, D.
submitted to the EMBL Data Library, September 1998
A/Reference number: Z21954
A/Accession: T41425
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-592 <WOO>
A/Cross-references: UNIPARC:UPI0000069B00; EMBL:AL031798; PIDN:CAA21194.1; GSPDB:GN00068
A/Experimental source: strain 972h-; cosmid c576
C/Genetics:
A/Gene: KSG1; SPC576.15C
A/Map position: 3
A/Introns: 191/3
C/Keywords: phosphotransferase

Query Match      79.7%; Score 63; DB 2; Length 592;
Best Local Similarity 75.0%; Pred. No. 0.0059;
Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      1 ANSFVGTAGYVSPELL 16
Db      269 SRSFVGTARYVSPVLL 284
: |||||:|||||

RESULT 6
C96549
hypothetical protein FLIM15.3 [imported] - Arabidopsis thaliana
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C/Accession: C96549
R/Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Hutzar, L.

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Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Matzli, H.
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salberg, S.L.; Schwartz, J.R.; Shum, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A66141; MUID:21016719; PMID:11130712
A:Accession: C96549
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-404 <STO>
A:Cross-references: UNIPROT:Q9SVB9; UNIPARC:UPI000009C93D; GB:AEO05173; NID:g4836928; PI
C:Genetics:
A:Gene: FILM15.3
A:Map position: 1
C:Superfamily: probable serine/threonine-specific protein kinase ATPK64; protein kinase

Query Match 77.2%; Score 61; DB 2; Length 404;
Best Local Similarity 62.5%; Pred. No. 0.0087;
Matches 10; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

OY 1 ANSFVGTQAVYSPKLL 16
:|||||:|:|:|:
Db 240 SNSFVGTDEYISPEVI 255

RESULT 7
T10202
hyprothetical protein P25G13.90 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C:Accession: T10202
R:Byan, M.; Pohl, T.; Weizenecker, T.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X.; Lemcke
submitted to the Protein Sequence Database, June 1999
A:Reference number: Z16991
A:Accession: T10202
A:Molecule type: DNA
A:Residues: 1-372 <BEV>
A:Cross-references: UNIPROT:Q9SV69; UNIPARC:UPI000000C5F3; EMBL:AL079349; GSPDB:GN00062;
A:Experimental source: cultivar Columbia; BAC clone F25G13
C:Genetics:
A:Gene: ATSP:F25G13.90
A:Map position: 4
C:Superfamily: kinase-related transforming protein; protein kinase homology

Query Match 75.9%; Score 60; DB 2; Length 372;
Best Local Similarity 62.5%; Pred. No. 0.012;
Matches 10; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

OY 1 ANSFVGTQAVYSPKLL 16
:|||||:|:|:|:
Db 226 SNSFVGTDEYISPEVI 241

RESULT 8
A45100
mitogen-activated protein kinase kinase (EC 2.7.1.-) 1, splice form A [validated] - huma
N:Alternate names: extracellular signal-regulated kinase activator kinase 1 (ERK kinase
N:Contains: MAP kinase kinase 1, splice form B; protein kinase (EC 2.7.1.37); protein-ty
C:Species: Homo sapiens (man)
C:Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: A45100; B45100; B46723; J02504
R:Seeger, R.; Seeger, D.; Lozman, F.J.; Ahn, N.G.; Graves, L.M.; Campbell, J.S.; Ericsson
J. Biol. Chem. 267, 25628-25631, 1992
A:Title: Human T-cell mitogen-activated protein kinase kinases are related to yeast sig
A:Reference number: A45100; MUID:93100262; PMID:1281467
A:Accession: A45100
A:Molecule type: mRNA; protein
A:Residues: 1-393 <SEG1>
A:Cross-references: UNIPROT:Q02750; UNIPARC:UPI000013BEC9; GB:L05624; NID:g188568; PIDN:
A:Experimental source: T-cells
A:Note: Sequence extracted from NCBI backbone (NCBIN:120827, NCBIPI:120828)

A:Accession: B45100
A:Molecule type: mRNA; protein
A:Residues: 1-146; 173-393 <SEG2>
A:Cross-references: UNIPARC:UPI000017251C; GB:L05624; NID:g188568
A:Experimental source: T-cells
A:Note: Sequence extracted from NCBI backbone (NCBIN:120837, NCBIPI:120838)
R:Zheng, C.F.; Guan, K.L.
J. Biol. Chem. 268, 11435-11439, 1993
A:Title: Cloning and characterization of two distinct human extracellular signal-regulat
A:Reference number: A46723; MUID:93266604; PMID:8388392
A:Accession: B46723
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-295, 'G', 296-393 <ZHE>
A:Cross-references: UNIPARC:UPI000017251D; GB:L11284; NID:g307183
A:Note: Sequence extracted from NCBI backbone (NCBIPI:132852)
R:Manour, S.U.; Resing, K.A.; Candi, J.M.; Hermann, A.S.; Gloor, J.W.; Herskind, K.R.;
J. Biochem. 116, 304-314, 1994
A:Title: Mitogen-activated protein (MAP) kinase phosphorylation of MAP kinase kinase: De
A:Reference number: J02504; MUID:95122457; PMID:7822248
A:Accession: J02504
A:Molecule type: protein
A:Residues: 5-96; 98-349; 354-393 <MAN>
A:Cross-references: UNIPARC:UPI000017251F; UNIPARC:UPI000017251F; UNIPARC:UPI0000172520
A:Note: phosphorylation sites determined in vitro
C:Comment: This enzyme is activated by protein kinase raf-1 (see PIR:A00637). It in turn
C:Genetics:
A:Gene: GDB:PRKML; MEK1, MAPKK1
A:Cross-references: GDB:136418; OMIM:176872
C:Complex: monomer
C:Function:
A:Description: catalyzes the formation of specific peptidyl-threonine-phosphate and pept
A:Pathway: MAP kinase cascade
C:Superfamily: kinase-related transforming protein; protein kinase homology
C:Keywords: alternative splicing; ATP; monomer; phosphoprotein; phosphotransferase; seri
F.1-1393/Product: MAP kinase kinase 1, splice form A #status experimental <MATA>
F.1-146; 173-393/Product: MAP kinase kinase 1, splice form B #status predicted <MATB>
F.166-361/Domain: protein kinase homology <KIN>
F.74-82/Region: protein kinase ATP-binding motif
F.97, 114, 190, 192/Active site: Lys, Glu, Asp, Lys #status predicted
F.218, 222/Binding site: phosphate (Ser) (covalent) (by raf-1 kinase) #status predicted
F.292, 366/Binding site: phosphate (Thr) (covalent) (by raf-1 kinase) #status experimenta

Query Match 75.9%; Score 60; DB 1; Length 393;
Best Local Similarity 75.0%; Pred. No. 0.013;
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 ANSFVGTQAVYSPKLL 16
:|||||:|:|:|:
Db 220 ANSFVGTQAVYSPKLL 235

RESULT 9
I59571
mitogen-activated protein kinase kinase (EC 2.7.1.-) 1, splice form A - mouse
N:Alternate names: ERK kinase 1; extracellular signal-regulated kinase activator kinase
N:Contains: Mus musculus (house mouse)
C:Species: Mus musculus (house mouse)
C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004
C:Accession: I59571; A46267; B46267; C46267; D46267; E46267
R:Crews, C.M.; Alessandrini, A.A.; Erikson, R.L.
Science 258, 478-480, 1992
A:Title: The primary structure of MEK, a protein kinase that phosphorylates and activate
A:Reference number: I59571; MUID:93030761; PMID:1411546
A:Accession: I59571
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-393 <RES>
A:Cross-references: UNIPROT:P31938; UNIPARC:UPI0000020B56; GB:L02526; NID:g191123; PIDN:
R:Crews, C.M.; Erikson, R.L.
Proc. Natl. Acad. Sci. U.S.A. 89, 8205-8209, 1992
A:Title: Purification of a murine protein-tyrosine/threonine kinase that phosphorylates
A:Reference number: A46267; MUID:92390415; PMID:1381507

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A/Accession: A46267
A/Molecule type: protein
A/Residues: 4-20;71-84;114-136;206-227;228-234;263-373; 'Q',375,'X',377-379,'X',381-384
A/Cross-references: UNIPARC:UPI0000175222; UNIPARC:UPI0000175224; UNIPARC:UPI0000175225;
A/Note: sequence modified after extraction from NCBI backbone
A/Note: sequence extracted from NCBI backbone (NCBI:P112867)
C/Complex: monomer
C/Function:
A/Description: catalyzes the formation of specific peptidyl-L-threonine-phosphate and pep-
A/Pathway: growth factor-stimulated cascade in which Raf-1, MAPKK, and MAPK are sequenti-
C/Superfamily: kinase-related transforming protein; protein kinase homology
C/Keywords: alternative splicing; ATP; phosphoprotein; phosphotransferase; serine/threon-
F:1-146;173-393/Product: mitogen-activated protein kinase kinase 1, splice form B #status
F:66-361/Domains: protein kinase homology <KIN>
F:74-82/Region: protein kinase ATP-binding motif
F:97,114,190,192/Active site: Lys, Glu, Asp, Lys #status predicted
F:292,386/Binding site: phosphate (Thr) (covalent) (by MAP kinase) #status predicted

Query Match 75.9%; Score 60; DB 1; Length 393;
Best Local Similarity 75.0%; Pred. No. 0.013;
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 ANSFVGTQAYVSPRL 16
Db 220 ANSFVGTQAYVSPRL 235

RESULT 10
JN0840
mitogen-activated protein kinase kinase (EC 2.7.1.-) 1, splice form A - rat
N/Alternate names: ERK kinase 1; extracellular signal-regulated kinase activator kinase
N/Contents: mitogen-activated protein kinase kinase 1B
C/Species: Rattus norvegicus (Norway rat)
C/Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004
C/Accession: JN0840; A47177; S29863; S32411
R:Wu, J.; Harrison, J.K.; Vincent, L.A.; Haystead, C.; Haystead, T.A.; Michel, H.; Hunt,
Gene 131, 303-304, 1993
A/Title: Cloning and sequencing of a cDNA encoding rat brain mitogen-activated protein
A/Reference number: JN0840; MUID:94010327; PMID:8406028
A/Accession: JN0840
A/Molecule type: mRNA
A/Residues: 1-393 <DOB>
A/Cross-references: UNIPROT:Q01986; UNIPARC:UPI0000168279; GB:X62313; NID:9407860; PIDN:
A/Accession: P00645
A/Molecule type: protein
A/Residues: 3-14;50-57;71-84;116-183 <DOB>
A/Cross-references: UNIPARC:UPI000004CBEQ; UNIPARC:UPI0000172521; UNIPARC:UPI0000172522;
R:Wu, J.; Harrison, J.K.; Vincent, L.A.; Haystead, C.; Haystead, T.A.; Michel, H.; Hunt,
Proc. Natl. Acad. Sci. U.S.A. 90, 173-177, 1993
A/Title: Molecular structure of a protein-tyrosine/chreonine kinase activating p42 mitog
A/Reference number: A47177; MUID:93126336; PMID:8380494
A/Accession: A47177
A/Molecule type: mRNA
A/Residues: 1-393 <WU1>
A/Cross-references: UNIPARC:UPI0000168279; GB:Z16415; NID:956628; PIDN:CAAT8905.1; PID:9
A/Experimental source: kidney
A/Note: sequence extracted from NCBI backbone (NCBI:N121997, NCBI:P121998)
R:Wu, J.
submitted to the EMBL Data Library, October 1992
A/Reference number: S29863
A/Accession: S29863
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-393 <WU1>
A/Cross-references: UNIPARC:UPI0000168279; EMBL:Z16415; NID:956628; PIDN:CAAT8905.1; PID
R:Osumi, M.; Terada, Y.; Okayama, H.
FEBS Lett. 320, 246-250, 1993
A/Title: Isolation of two members of the rat MAP kinase kinase gene family.
A/Reference number: S32411; MUID:93215844; PMID:8462694
A/Accession: S32411
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-393 <OTS>

```

```

A/Cross-references: UNIPARC:UPI0000168279; EMBL:D14591; NID:9286228; PIDN:BA03441.1; PII
C/Complex: monomer
C/Function:
A/Description: catalyzes the formation of specific peptidyl-L-threonine-phosphate and pep-
A/Pathway: growth factor-stimulated cascade in which Raf-1, MAPKK, and MAPK are sequenti-
C/Superfamily: kinase-related transforming protein; protein kinase homology
C/Keywords: alternative splicing; ATP; phosphoprotein; phosphotransferase; serine/threon-
F:1-146;173-393/Product: mitogen-activated protein kinase kinase 1, splice form B #status
F:66-361/Domains: protein kinase homology <KIN>
F:74-82/Region: protein kinase ATP-binding motif
F:97,114,190,192/Active site: Lys, Glu, Asp, Lys #status predicted
F:292,386/Binding site: phosphate (Thr) (covalent) (by MAP kinase) #status predicted

Query Match 75.9%; Score 60; DB 1; Length 393;
Best Local Similarity 75.0%; Pred. No. 0.013;
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 ANSFVGTQAYVSPRL 16
Db 220 ANSFVGTQAYVSPRL 235

RESULT 11
S42068
mitogen-activated protein kinase kinase (EC 2.7.1.-) 1, splice form A - rabbit
N/Alternate names: ERK kinase 1; extracellular signal-regulated kinase activator kinase 1
N/Contents: mitogen-activated protein kinase kinase 1B
C/Species: Oryctolagus cuniculus (domestic rabbit)
C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C/Accession: S42068
R:Ashworth, A.
submitted to the EMBL Data Library, February 1994
A/Description: cDNA sequence of rabbit MAP kinase kinase 1.
A/Reference number: S42068
A/Accession: S42068
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-393 <ASH>
A/Cross-references: UNIPROT:P29678; UNIPARC:UPI000016C587; EMBL:Z30163; NID:9456201; PIDN
C/Complex: monomer
C/Function:
A/Description: catalyzes the formation of specific peptidyl-L-threonine-phosphate and pep-
A/Pathway: growth factor-stimulated cascade in which Raf-1, MAPKK, and MAPK are sequenti-
C/Superfamily: kinase-related transforming protein; protein kinase homology
C/Keywords: alternative splicing; ATP; phosphoprotein; phosphotransferase; serine/threon-
F:1-146;173-393/Product: mitogen-activated protein kinase kinase 1, splice form B #status
F:66-361/Domains: protein kinase homology <KIN>
F:74-82/Region: protein kinase ATP-binding motif
F:97,114,190,192/Active site: Lys, Glu, Asp, Lys #status predicted
F:292,386/Binding site: phosphate (Thr) (covalent) (by MAP kinase) #status predicted

Query Match 75.9%; Score 60; DB 1; Length 393;
Best Local Similarity 75.0%; Pred. No. 0.013;
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 ANSFVGTQAYVSPRL 16
Db 220 ANSFVGTQAYVSPRL 235

RESULT 12
S46361
mitogen-activated protein kinase kinase (EC 2.7.1.-) 1, splice form A - Chinese hamster
N/Alternate names: ERK kinase 1; extracellular signal-regulated kinase activator kinase 1
N/Contents: mitogen-activated protein kinase kinase 1B
C/Species: Cricetus griseus (Chinese hamster)
C/Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C/Accession: S46361
R:Pages, G.; Brunet, A.; L'Allemain, G.; Polysegur, J.
EMBO J. 13, 3003-3010, 1994
A/Title: Constitutive mutant and putative regulatory serine phosphorylation site of mamme
A/Reference number: S46361; MUID:94313981; PMID:8039496
A/Accession: S46361

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A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-393 <PAC>
A:Cross-references: UNIPROT:Q63980; UNIPARC:UPI000012F481; GB:S70933; NID:g547336; PIDN:
C:Function:
A:Description: catalyzes the formation of specific peptidyl-threonine-phosphate and pept
A:Pathway: growth factor-stimulated cascade in which Raf-1, MAPKK, and MAPK are sequenti
C:Superfamily: kinase-related transforming protein; protein kinase homology
C:Keywords: alternative splicing; ATP; phosphoprotein; phosphotransferase; serine/threon
F:1-146/173-393/Product: mitogen-activated protein kinase kinase 1, splice form B #statu
F:66-366/Domain: protein kinase homology <KIN>
F:74-82/Region: protein kinase ATP-binding motif
F:97-114,150,192/Active site: Lys, Glu, Asp, Lys #status predicted
F:388/Binding site: phosphate (Thr) (covalent) (by MAP kinase) #status experimental

Query Match          75.9%; Score 60; DB 1; Length 393;
Best Local Similarity 75.0%; Pred. No. 0.013;
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Cy 1 ANSFVGTAGVSPRL 16
Db 220 ANSFVGTSTYSPRL 235

RESULT 13
A45176
protein kinase Docr1 - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 30-Apr-1993 #sequence_revision 30-Apr-1993 #text_change 09-Jul-2004
C:Accession: A45176
R:Tsuda, L.; Inoue, Y.H.; Yoo, M.A.; Mizuno, M.; Hata, M.; Lim, Y.M.; Adachi-Yamada, T.;
Cell 72, 407-414, 1993
A:Title: A protein kinase similar to MAP kinase activator acts downstream of the raf kin
A:Reference number: A45176; MUID:93151415; PMID:8381718
C:Accession: A45176
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-393 <TSU>
A:Cross-references: UNIPROT:Q24324; UNIPARC:UPI0000129906
A:Note: sequence extracted from NCBI backbone (NCBI:124867)
C:Superfamily: kinase-related transforming protein; protein kinase homology
F:82-361/Domain: protein kinase homology <KIN>

Query Match          75.9%; Score 60; DB 2; Length 393;
Best Local Similarity 75.0%; Pred. No. 0.013;
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Cy 1 ANSFVGTAGVSPRL 16
Db 236 ANSFVGTSTYSPRL 251

RESULT 14
S36186
mitogen-activated protein kinase kinase (EC 2.7.1.-) 1 - African clawed frog
N:Alternate names: ERK kinase 1; extracellular signal-regulated kinase activator kinase
C:Species: Xenopus laevis (African clawed frog)
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C:Accession: S36186; S37632; S23389
R:Kosako, H.; Nishida, E.; Gotoh, Y.
EMBO J. 12, 787-794, 1993
A:Title: cDNA cloning of MAP kinase kinase reveals kinase cascade pathways in yeasts to
A:Reference number: S36186; MUID:93178455; PMID:8440264
A:Accession: S36186
A:Molecule type: mRNA
A:Residues: 1-395 <KOS>
A:Cross-references: UNIPROT:Q05116; UNIPARC:UPI000008433; EMBL:D13700; NID:g222964; PID
A:Accession: S37632
A:Molecule type: Protein
A:Residues: 2-20/37-47; 71-84; 169-177; 186-214; 282-287; 317-324; 327-341; 356-363 <KO2>
A:Cross-references: UNIPARC:UPI0000172529; UNIPARC:UPI000017252A; UNIPARC:UPI000017252B;
530; UNIPARC:UPI0000172531; UNIPARC:UPI0000172532

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R:Kosako, H.; Gotoh, Y.; Matsuda, S.; Ishikawa, M.; Nishida, E.
EMBO J. 11, 2903-2908, 1992
A:Title: Xenopus MAP kinase activator is a serine/threonine/tyrosine kinase activated by
A:Reference number: S23389; MUID:92347324; PMID:11322292
A:Accession: S23389
A:Molecule type: Protein
A:Residues: 186-203, 'X', 205-206, 'X', 208-214 <KO3>
A:Cross-references: UNIPARC:UPI00000F83EE
C:Complex: monomer
C:Function:
A:Description: catalyzes the formation of specific peptidyl-threonine-phosphate and pept
A:Pathway: growth factor-stimulated cascade in which Raf-1, MAPKK, and MAPK are sequenti
C:Superfamily: kinase-related transforming protein; protein kinase homology
C:Keywords: ATP; phosphoprotein; phosphotransferase; serine/threonine/tyrosine-specific
F:2-395/Product: mitogen-activated protein kinase kinase #status experimental <MAT>
F:66-363/Domain: protein kinase homology <KIN>
F:74-82/Region: protein kinase ATP-binding motif
F:97-114,150,192/Active site: Lys, Glu, Asp, Lys #status predicted
F:388/Binding site: phosphate (Thr) (covalent) (by MAP kinase) #status predicted

Query Match          75.9%; Score 60; DB 1; Length 395;
Best Local Similarity 75.0%; Pred. No. 0.013;
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Cy 1 ANSFVGTAGVSPRL 16
Db 220 ANSFVGTSTYSPRL 235

RESULT 15
S41054
mitogen-activated protein kinase kinase (EC 2.7.1.-) 2 - common carp
N:Alternate names: ERK kinase 2; extracellular signal-regulated kinase activator kinase
C:Species: Cyprinus carpio (common carp)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C:Accession: S41054
R:Huang, C.J.; Lee, M.S.; Chang, G.D.; Huang, F.L.; Lo, T.B.
Biochim. Biophys. Acta 1220, 223-225, 1994
A:Title: Molecular cloning and sequencing of a carp cDNA encoding mitogen-activated prot
A:Reference number: S41054; MUID:94146120; PMID:8312367
A:Accession: S41054
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-397 <HNA>
A:Cross-references: UNIPROT:Q90321; UNIPARC:UPI000012F488; EMBL:L23935; NID:g397677; PID
C:Function:
A:Description: catalyzes the formation of specific peptidyl-threonine-phosphate and pept
A:Pathway: growth factor-stimulated cascade in which Raf-1, MAPKK, and MAPK are sequenti
C:Superfamily: kinase-related transforming protein; protein kinase homology
C:Keywords: ATP; phosphoprotein; phosphotransferase; serine/threonine/tyrosine-specific
F:67-366/Domain: protein kinase homology <KIN>
F:75-83/Region: protein kinase ATP-binding motif
F:98-115,191,193/Active site: Lys, Glu, Asp, Lys #status predicted
F:391/Binding site: phosphate (Thr) (covalent) (by MAP kinase) #status predicted

Query Match          75.9%; Score 60; DB 1; Length 397;
Best Local Similarity 75.0%; Pred. No. 0.013;
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Cy 1 ANSFVGTAGVSPRL 16
Db 221 ANSFVGTSTYSPRL 236

Search completed: May 16, 2006, 13:28:31
Job time : 39 secs

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GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: May 17, 2006, 11:46:44 ; Search time 194 Seconds

(without alignments)
37.709 Million cell updates/sec

Title: US-10-689-576-3

Sequence: 1 ANSFVGTAAQVSPPELL 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

A_Geneseq 8 : *
1: geneseqp1980s : *
2: geneseqp1990s : *
3: geneseqp2000s : *
4: geneseqp2001s : *
5: geneseqp2002s : *
6: geneseqp2003as : *
7: geneseqp2003bs : *
8: geneseqp2004s : *
9: geneseqp2005s : *
10: geneseqp2006s : *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	79	100.0	16	2	AAW71727
2	79	100.0	19	9	ADV13389 Human pho
3	79	100.0	25	3	AAI13202
4	79	100.0	98	3	AAI13213
5	79	100.0	285	8	ABR57461
6	79	100.0	289	8	ADJ38865
7	79	100.0	319	6	ABU04709
8	79	100.0	319	6	ABU04720
9	79	100.0	335	4	AAI13202
10	79	100.0	335	8	ADJ38895
11	79	100.0	361	9	ADY85535
12	79	100.0	462	10	AEF60044
13	79	100.0	468	6	ABU04719
14	79	100.0	468	6	ABU04705
15	79	100.0	506	6	AAI13202
16	79	100.0	506	6	ABU04715
17	79	100.0	535	4	AAI13202
18	79	100.0	535	6	ABU04713
19	79	100.0	556	2	AAI13202
20	79	100.0	556	2	AAI13202
21	79	100.0	556	2	AAI13202
22	79	100.0	556	3	AAI13202
23	79	100.0	556	3	AAI13202

24	79	100.0	556	3	AAI13202
25	79	100.0	556	6	ABU04708
26	79	100.0	556	6	ABU04718
27	79	100.0	556	6	ABU04718
28	79	100.0	556	6	ABU04712
29	79	100.0	556	6	ABU04712
30	79	100.0	556	6	ABU04712
31	79	100.0	556	6	ABU04712
32	79	100.0	556	6	ABU04714
33	79	100.0	556	6	ABU04707
34	79	100.0	556	6	ABU04717
35	79	100.0	556	7	ABM79012
36	79	100.0	556	7	ADD44919
37	79	100.0	556	7	ADD44915
38	79	100.0	556	7	ADD89983
39	79	100.0	556	8	ADI36055
40	79	100.0	556	8	ADI36055
41	79	100.0	556	8	ADI36055
42	79	100.0	559	7	ADD44917
43	79	100.0	559	7	ADD44913
44	79	100.0	559	8	ABM84519
45	71	89.9	473	8	ADJ24198

ALIGNMENTS

RESULT 1	AAW71727 standard; peptide: 16 AA.
ID	AAW71727
AC	AAW71727;
DT	10-DEC-1998 (first entry)
DE	3-phosphoinositide-dependent protein kinase peptide #1.
XX	Protein kinase B-alpha; 3-phosphoinositide-dependent protein kinase;
XX	diabetes; cancer; cell proliferation; phosphorylation.
XX	Homo sapiens.
XX	OS
XX	WO9841638-A1.
XX	24-SEP-1998.
XX	16-MAR-1998; 98WO-GB000777.
XX	17-MAR-1997; 97GB-00005462.
XX	19-JUN-1997; 97GB-00012826.
XX	15-AUG-1997; 97GB-00017253.
XX	03-OCT-1997; 97US-00943667.
XX	(MEDI-) MEDICAL RES COUNCIL.
XX	Allesi DR;
XX	WPI; 1998-531572/45.
XX	New isolated 3-phosphoinositide-dependent protein kinase - which
XX	phosphorylates and activates protein kinase B-alpha, used to develop
XX	products for treating diabetes or cancers or for enhancing cell
XX	proliferation.
XX	Claim 9; Page 91; 120pp; English.
XX	A pure 3-phosphoinositide-dependent protein kinase (3PDK) that
XX	phosphorylates and activates PK B-alpha has been isolated. The present
XX	sequence represents a peptide from the 3PDK. Products from the present
XX	invention (e.g. 3PDK, nucleotide sequence encoding 3PDK, antibodies
XX	against 3PDK) can be used to identify compounds which modulate the PK
XX	activity e.g. for treating diabetes or cancers or for enhancing cell
XX	proliferation in the regeneration of nerves or in wound healing

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XX Sequence 16 AA;
SQ
Query Match 100.0%; Score 79; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 5e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ANSFVGTQAYVSPPELL 16
Db 1 ANSFVGTQAYVSPPELL 16

RESULT 2
ADV13389 ID ADV13389 standard; peptide: 19 AA.
XX ADV13389;
AC
XX 10-MAR-2005 (first entry)
DT
XX Human phosphorylated peptide from phosphoprotein #1327.
DE
XX Alzheimer's disease; neuroprotective; nootropic; degeneration; tumor;
XX neoplasm; neurological disease; phosphorylation; protein sequencing;
XX phosphoprotein.
OS Homo sapiens.
XX
XX WO2004108948-A2.
XX
XX 16-DEC-2004.
XX
XX 04-JUN-2004; 2004WO-US017613.
XX
XX 04-JUN-2003; 2003JUS-0476010P.
XX
XX (HARD ) HARVARD COLLEGE.
XX
XX Gysi SP;
XX
XX WPI; 2005-031720/03.
XX
XX Characterizing phosphorylated polypeptides in a sample comprises
XX digesting the polypeptides with a protease thus generating test peptides,
XX and collecting a fraction of test peptides that enriched for positively
XX charged peptides.
XX
XX Claim 16; Page 85; 123pp; English.
XX
XX The invention relates to characterizing phosphorylated polypeptides in a
XX sample comprising digesting the polypeptides with a protease thus
XX generating test peptides, and collecting a fraction of test peptides that
XX enriched for positively charged peptides. Also included are a method
XX (comprising determining the presence, absence or level of one ore more
XX phosphorylated peptides as identified above in cells having a cell state
XX and determining the degree of correlation between the presence, absence
XX or level of phosphorylated polypeptide with the cell state), an isolated
XX peptide of 5-50 amino acids comprising an amino acid sequence that is a
XX subsequence of any of the protein sequences given in the specification,
XX and which comprise a phosphorylation site within the subsequence), an
XX isolated polypeptide selected from any of the polypeptides listed in the
XX specification and is modified at a modification site, an isolated peptide
XX comprising a mass spectral peak signatures, a method for identifying a
XX treatment that modulates phosphorylation of an amino acid in a target
XX polypeptide, a method for generating a peptide standard, a pair of
XX peptide standards comprising the peptide obtained (where the peptide is
XX phosphorylated and a corresponding peptide comprising an identical amino
XX acid sequence but which is not phosphorylated), a system (comprising a
XX computer memory comprising data files storing information relating to the
XX identifying characteristics of positively charged peptides, and a data
XX analysis module capable of executing instructions for organizing and/or
XX searching the data files), a computer program product (comprising data
XX relating to the identifying characteristics of positively charged

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CC peptides and comprising instructions for organizing and/or searching the
CC data), and a method for identifying N-terminal peptides in a sample. The
CC method is useful for characterizing phosphorylated polypeptides in a
CC sample. The present sequence is a peptide from a human phosphoprotein,
CC containing a phosphorylation site, identified by the method of the
CC invention.
XX
XX Sequence 19 AA;
SQ
Query Match 100.0%; Score 79; DB 9; Length 19;
Best Local Similarity 100.0%; Pred. No. 6.1e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ANSFVGTQAYVSPPELL 16
Db 1 ANSFVGTQAYVSPPELL 16

RESULT 3
AAB13202 ID AAB13202 standard; peptide: 25 AA.
XX AAB13202;
AC
XX 11-JAN-2001 (first entry)
DT
XX Mammalian PDK domain #5.
DE
XX
XX Human; mouse; PDK domain; pdk-1; AKT kinase; daf-18;
XX insulin signalling pathway; daf-2; age-1; insulin receptor; PI 3-Kinase;
XX PKB kinase; PTEN lipid phosphatase; antidiabetic; anorectic; obesity;
XX diabetes.
XX
XX Homo sapiens.
XX
XX Mus musculus.
XX
XX WO200033068-A1.
XX
XX 08-JUN-2000.
XX
XX 02-DEC-1999; 99WO-US028529.
XX
XX 03-DEC-1998; 98US-00205658.
XX
XX (GENO ) GEN HOSPITAL CORP.
XX
XX Ruvkun G, Ogg S;
XX
XX WPI; 2000-423022/36.
XX
XX Diagnosing and treating obesity and impaired glucose tolerance using
XX modulators of daf-18 expression and/or activity.
XX
XX Disclosure; Page 359; 402pp; English.
XX
XX The present sequence is a domain of mammalian PKX which shows homology to
XX pdk-1 from Caenorhabditis elegans. A number of C. elegans genes have been
XX identified as homologues of genes in the mammalian insulin signalling
XX pathway. The C. elegans age-1 gene encodes a homologue of the mammalian
XX PI 3-kinase whilst daf-2 encodes a homologue of the mammalian insulin
XX receptor. The C. elegans AKT kinase and PKB kinase act downstream of daf-
XX 2 and age-1, just as their mammalian homologues act downstream of insulin
XX signalling. The C. elegans PTEN lipid phosphatase homologue, DAF-18, has
XX been found to act upstream of AKT in the pathway. This discovery has
XX enabled mammalian PTEN action to be mapped to the insulin signalling
XX pathway. Conserved DAF motifs can be used to design probes to identify
XX mammalian DAF homologues and thus to identify individuals with a
XX predisposition toward the development of glucose intolerance conditions,
XX such as obesity and diabetes
XX
XX Sequence 25 AA;
SQ
Query Match 100.0%; Score 79; DB 3; Length 25;

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Best Local Similarity 100.0%; Pred. No. 8,4e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ANSFVGTAGYVSPPELL 16
|||
Db 8 ANSFVGTAGYVSPPELL 23

RESULT 4
AAB13213
ID AAB13213 standard; protein; 98 AA.

XX AC AAB13213;

XX DT 11-JAN-2001 (first entry)

XX DE Human PDK domain #3.

XX KW Human; PDK domain; pdk-1; AKT kinase; daf-18; insulin signalling pathway;

KW daf-2; age-1; insulin receptor; PI 3-kinase; PKB kinase;

KW PTEN lipid phosphatase; antidiabetic; anorectic; obesity; diabetes.

XX OS Homo sapiens.

XX PN W0200033068-A1.

XX PD 08-JUN-2000.

XX PF 02-DEC-1999; 99WO-US028529.

XX PR 03-DEC-1998; 98US-00205658.

XX PA (GENO) GEN HOSPITAL CORP.

XX PI Ruvkun G, Ogg S;

XX DR WPI; 2000-423022/36.

XX PT Diagnosing and treating obesity and impaired glucose tolerance using

XX PS modulators of daf-18 expression and/or activity.

XX PS Disclosure; Page 362; 402pp; English.

XX CC The present sequence is a human PDK domain which shows homology to pdk-1

CC from Caenorhabditis elegans. A number of C. elegans genes have been

CC identified as homologues of genes in the mammalian insulin signalling

CC pathway. The C. elegans age-1 gene encodes a homologue of the mammalian

CC PI 3-kinase whilst daf-2 encodes a homologue of the mammalian insulin

CC receptor. The C. elegans AKT kinase and PKB kinase act downstream of daf-

CC 2 and age-1, just as their mammalian homologues act downstream of insulin

CC signalling. The C. elegans PTEN lipid phosphatase homologue, DAF-18, has

CC been found to act upstream of AKT in the pathway. This discovery has

CC enabled mammalian PTEN action to be mapped to the insulin signalling

CC pathway. Conserved DAF motifs can be used to design probes to identify

CC mammalian DAF homologues and thus to identify individuals with a

CC predisposition toward the development of glucose intolerance conditions,

CC such as obesity and diabetes

XX SQ Sequence 98 AA;

XX Query Match 100.0%; Score 79; DB 3; Length 98;

XX Best Local Similarity 100.0%; Pred. No. 4e-06;

XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ANSFVGTAGYVSPPELL 16

|||

Db 7 ANSFVGTAGYVSPPELL 22

RESULT 5

ABR57461

ID ABR57461 standard; protein; 285 AA.

AC ABR57461;

XX DT 15-SEP-2003 (first entry)

XX DE AGC family protein kinase protein PDK1.

XX KW Protein kinase B; PKB/Akt; enzyme; crystal structure; drug discovery;

KW protein co-ordinate data; cytostatic; antidiabetic; vasotropic; PKB;

KW neurotrophic; neuroprotective; gene therapy; protein kinase B beta; PRKBeta;

KW structural analysis; cancer; diabetes; erectile dysfunction;

XX KW neurodegeneration.

XX OS Unidentified.

XX PN W02003016516-A2.

XX PD 27-FEB-2003.

XX PF 14-AUG-2002; 2002WO-GB003735.

XX PR 14-AUG-2001; 2001GB-00019860.

XX PR 01-MAY-2002; 2002GB-00009985.

XX PA (NOVS) NOVARTIS FORSCHUNGSSTIFTUNG ZWEIGNIEDERL.

XX PA (CANC-) CANCER RES INST.

XX PI Barford D, Yang J, Hemmings BA, Cron PD;

XX DR WPI; 2003-268328/26.

XX PT New crystal of protein kinase B beta, useful for activating protein

XX PT kinases, e.g. AGC kinases, comprises three-dimensional atomic coordinates

XX PT or a tetragonal space group.

XX PS Disclosure; Fig 4; 284pp; English.

XX CC The present invention describes a crystal of protein kinase B beta

CC (PRKBeta) comprising (I), where (I) comprises: (a) a tetragonal space

CC group P4-1-2-1-2 and unit cell dimensions of: a = 149.33 plus or minus

CC 0.5 Angstrom, b = 149.33 plus or minus 0.5 Angstrom, c = 39.77 plus or

CC minus 0.5 Angstrom; a = 148.40 plus or minus 0.5 Angstrom, b = 148.40

CC plus or minus 0.5 Angstrom, c = 38.55 plus or minus 0.5 Angstrom; a =

CC 149.70 plus or minus 0.5 Angstrom, b = 149.70 plus or minus 0.5 Angstrom,

CC c = 39.19 plus or minus 0.5 Angstrom; or a = 149.52 plus or minus 0.5

CC Angstrom, b = 149.52 plus or minus 0.5 Angstrom, c = 39.06 plus or minus

CC 0.5 Angstrom; or (b) the three-dimensional atomic coordinates listed in

CC the specification. (I) has cytosolic, antidiabetic, vasotropic,

CC neurotrophic and neuroprotective activities, and can be used in gene

CC therapy. The crystal of PRKBeta, and methods from the present invention,

CC are useful in activating protein kinases, particularly AGC kinases, for

CC identifying modulators of protein kinase activity, and for structural

CC analysis of other protein kinases. The crystal may also be used in

CC manufacturing a medicament for treating cancers, diabetes, erectile

CC dysfunction or neurodegeneration. The present sequence represents an AGC

CC family protein kinase which is given in the exemplification of the

CC present invention

XX SQ Sequence 285 AA;

XX Query Match 100.0%; Score 79; DB 6; Length 285;

XX Best Local Similarity 100.0%; Pred. No. 1.4e-05;

XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ANSFVGTAGYVSPPELL 16

|||

Db 164 ANSFVGTAGYVSPPELL 179

RESULT 6

ADJ38865

ID ADJ38865 standard; protein; 289 AA.

XX AC ADJ38865;

XX 06-MAY-2004 (first entry)
 XX PDK1 amino acid sequence.
 XX phosphoinositide dependent protein kinase 1; PDK1, molecular modelling;
 XX protein kinase; catalytic domain; enzyme; hydrophobic pocket;
 XX insulin signalling pathway; signalling; crystalline form;
 XX protein co-ordinate data; three-dimensional structure; antifungal;
 XX antidiabetic; cardiant; cytosolic; cerebroprotective; vasotropic;
 XX anorectic; protein kinase modulator; cancer; diabetes; obesity;
 XX apoptosis inhibition; ischaemia disease; stroke; myocardial infarction;
 XX neural injury.
 XX Unidentified.
 XX WO2003104481-A2.
 XX 18-DEC-2003.
 XX 09-JUN-2003; 2003MO-GB002509.
 XX 08-JUN-2002; 2002GB-00013186.
 XX (UYDU-) UNIV DUNDEE.
 XX Alessi D, Biondi R, Komander D, Van AD;
 XX WPI; 2004-062373/06.
 XX Selecting/designing compound for modulating activity of phosphoinositide
 XX dependent protein kinase 1 by using molecular modelling to select/design
 XX compound predicted to interact with protein kinase catalytic domain.
 XX Example 1; Fig 3; 383pp; English.
 XX The present invention describes a method (M1) for selecting or designing
 XX a compound for modulating the activity of phosphoinositide dependent
 XX protein kinase 1 (PDK1) comprising using molecular modelling means to
 XX select or design a compound that is predicted to interact with the
 XX protein kinase catalytic domain of PDK1, and selecting a compound that is
 XX predicted to interact with the protein kinase catalytic domain. Also
 XX described: (1) selecting or designing (M2) a compound for modulating the
 XX activity of a hydrophobic pocket (PIF binding pocket)-containing protein
 XX kinase having a hydrophobic pocket in the position equivalent to the
 XX hydrophobic pocket of human PDK1 that is defined by residues including
 XX Lys115, Ile118, Ile119, Val124, Val127 and/or Leu155 of full-length human
 XX PDK1 and further having a phosphate binding pocket in the position
 XX equivalent to the phosphate binding pocket of human PDK1 that is defined
 XX by residues including Lys76, Arg131, Thr148 and/or Gln150; (2) assessing
 XX (M3) the activation state of a structure for a protein kinase; (3) a
 XX mutated protein kinase (1); (4) a polynucleotide (II) encoding (1); (5) a
 XX host cell (III) comprising (II); (6) identifying (M4) a compound that
 XX modulates the protein kinase activity of a protein kinase (e.g., PDK1);
 XX (7) an antibody (IV) reactive with the phosphate binding pocket of PDK1
 XX or (1) or an antibody reactive with PDK1 or (1) but not with the protein
 XX kinase mutated at the phosphate binding site, or vice versa; (8) a
 XX compound (V) identified or identifiable by (M1) or (M3); (9) use of (V),
 XX (1), (II) in medicine; (10) use of (V), (1), (II) for the manufacture of
 XX a medicament for the treatment of a patient in need of modulation of
 XX signalling by a protein kinase as defined, for example PDK1, SGK, PKB, or
 XX p70 S6 kinase, for example insulin signalling pathway and/or
 XX PDK1/PDK2/SGK/PKB/p70 S6 kinase/PRK2/PRK signalling, and (11) a
 XX crystalline form (VI) of polypeptide as defined in (M1). (1) has
 XX antifungal, antidiabetic, cardiant, cytosolic, cerebroprotective,
 XX vasotropic and anorectic activities, and can be used as a modulator of
 XX protein kinase. (V) is useful for modulating the ability of protein
 XX kinase to phosphorylate different substrates, e.g. different naturally
 XX occurring polypeptides, to different extents. (V) inhibits or increases
 XX the activity of protein kinase. The protein structures e.g., the co-
 XX ordinate as provided in the specification are useful for designing
 XX reagent useful in drug designing assays or characterisation of protein
 XX kinase activity or regulation. (V) capable of producing the activity of

CC PKC, e.g., PKC beta, PRK1 or PRK2, PDK1, PKB, SGK or p70 S6 kinase, is
 CC useful in treating cancer. (V) capable of increasing the activity of
 CC PDK1, PKB, SGK or p70 S6 kinase is useful in treating diabetes or obesity
 CC or may be useful in inhibiting apoptosis, thus useful in treating
 CC diseases in which apoptosis is involved e.g., mechanical (including heart)
 CC tissue injury or ischaemia disease such as stroke, myocardial infarction
 CC and neural injury. (V) is useful as an antifungal agent. The present
 CC sequence is used in the exemplification of the present invention.
 XX Sequence 289 AA;
 SQ
 Query Match 100.0%; Score 79; DB 8; Length 289;
 Best Local Similarity 100.0%; Pred. No. 1,4e-05;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ANSFVGTGAQYVSPDLL 16
 Db 169 ANSFVGTGAQYVSPDLL 184
 RESULT 7
 ID ABU04709 standard; protein; 319 AA.
 XX
 AC ABU04709;
 XX
 DT 29-JAN-2003 (first entry)
 XX
 DE Human expressed protein tag (EPT) #1375.
 XX
 KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
 KW protease; protease inhibitor; transporter; cytoskeletal protein;
 KW receptor; transcription factor; cancer; MHC;
 KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
 KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukemia.
 XX
 OS Homo sapiens.
 XX
 PN NO200278524-A2.
 XX
 PD 10-OCT-2002.
 XX
 PF 28-MAR-2002; 2002MO-US009671.
 XX
 PR 28-MAR-2001; 2001US-0279495P.
 PR 21-MAY-2001; 2001US-0292544P.
 PR 08-AUG-2001; 2001US-0310801P.
 PR 01-OCT-2001; 2001US-0326370P.
 PR 04-DEC-2001; 2001US-0336780P.
 PR 20-FEB-2002; 2002US-0358985P.
 XX
 PA (ZYCO-) ZYCOS INC.
 PI Chicz RM, Tomlinson AJ, Urban RG;
 XX
 DR WPI; 2003-040607/03.
 XX
 XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
 XX cytoskeletal proteins, receptors or transcription factors), useful for
 XX treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
 XX leukemia.
 XX
 PS Example 2; SEQ ID NO 1375; 134pp; English.
 XX
 XX The invention describes a purified polypeptide, which comprises a
 XX fragment of a kinase, phosphatase, protease, protease inhibitor,
 XX transporter, cytoskeletal protein, receptor or transcription factor. The
 XX polypeptide is useful as an immunogenic composition for eliciting in a
 XX mammal an immunogenic response directed against any of the purified
 XX polypeptide. The purified polypeptide, or the antibody that binds to this
 XX polypeptide, is useful for treating cancer. The polypeptide is also
 XX useful for identifying compounds that binds to a naturally processed
 XX class I or class II MHC-binding polypeptide. The polypeptides and

CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX
SQ Sequence 319 AA;

Query Match 100.0%; Score 79; DB 6; Length 319;
Best Local Similarity 100.0%; Pred. No. 1.6e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ANSFGVGTAGVYSPRL 16
|||
Db 2 ANSFGVGTAGVYSPRL 17

RESULT 8
ABU04720
ID ABU04720 standard; protein; 319 AA.
XX
AC ABU04720;
XX
DT 29-JAN-2003 (first entry)
XX
DE Human expressed protein tag (EPT) #1386.
XX
KM Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KM protease; protease inhibitor; transporter; cytoskeletal protein;
KM receptor; transcription factor; cancer; MHC;
KM major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KM adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX
OS Homo sapiens.
XX
PN WO200278524-A2.
XX
PD 10-OCT-2002.
XX
PF 28-MAR-2002; 2002WO-US009671.
XX
PR 28-MAR-2001; 2001US-0279495P.
PR 21-MAY-2001; 2001US-0292544P.
PR 08-AUG-2001; 2001US-0310801P.
PR 01-OCT-2001; 2001US-0326370P.
PR 04-DEC-2001; 2001US-0336780P.
PR 20-FEB-2002; 2002US-0358985P.
XX
PA (ZYCO-) ZYCOS INC.
XX
PI Chicx RM, Tomlinson AJ, Urban RG;
XX
DX WPI; 2003-040607/03.
XX
PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukaemia.
XX
XX
XX Example 2; SEQ ID NO 1386; 134pp; English.
PS
XX The invention describes a purified polypeptide, which comprises a
XX fragment of a kinase, phosphatase, protease, protease inhibitor,
XX transporter, cytoskeletal protein, receptor or transcription factor. The
XX polypeptide is useful as an immunogenic composition for eliciting in a
XX mammal an immunogenic response directed against any of the purified
XX polypeptide. The purified polypeptide, or the antibody that binds to this
XX polypeptide, is useful for treating cancer. The polypeptide is also
XX useful for identifying compounds that binds to a naturally processed
XX class I or class II MHC-binding polypeptide. The polypeptides and

CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX
SQ Sequence 319 AA;

Query Match 100.0%; Score 79; DB 6; Length 319;
Best Local Similarity 100.0%; Pred. No. 1.6e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ANSFGVGTAGVYSPRL 16
|||
Db 2 ANSFGVGTAGVYSPRL 17

RESULT 9
AAB99847
ID AAB99847 standard; protein; 335 AA.
XX
AC AAB99847;
XX
DT 20-SEP-2001 (first entry)
XX
DE AGC protein kinase family member PDK1 protein sequence.
XX
KM Protein kinase; identification; hydrophobic pocket; interacting; cancer;
KM diabetes; inhibition; apoptosis; tissue injury; ischemic injury; stroke.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200144497-A2.
XX
PD 21-JUN-2001.
XX
PF 04-DEC-2000; 2000WO-GB004598.
XX
PR 02-DEC-1999; 99US-0168559P.
XX
PA (UYDU-) UNIV DUNDEE.
XX
PI Alessi D, Biondi R;
XX
DX WPI; 2001-390252/41.
XX
PT Identifying modulators of protein kinase (PK) activity, useful in
PT developing drugs for treating cancer or diabetes, by measuring the
PT ability of the compound to modulate or mimic the interaction of PK with
PT interacting polypeptides.
XX
XX
XX Disclosure; Fig 16; 180pp; English.
PS
XX
XX The present invention describes a method for identifying a compound that
XX modulates protein kinase activity. The method comprises measuring the
XX ability of the compound to inhibit, promote or mimic the interaction of a
XX hydrophobic pocket-containing protein kinase with an interacting
XX polypeptide. The interacting polypeptide interacts with the hydrophobic
XX pocket of the protein kinase and/or comprises the amino acid sequence
XX Phe/Tyr-Xaa-Xaa-Phe/Tyr (1). The method is useful in screening assays for
XX developing pharmaceutical compounds or drugs. Compounds, polypeptides or
XX polynucleotides from the present invention are useful in medicine,
XX particularly in the manufacture of a medicament for treating a patient in
XX need of modulation of signalling by a hydrophobic pocket-containing
XX protein kinase. Specifically, the patient has cancer or diabetes or is in
XX need of inhibition of apoptosis, e.g. a patient suffering from tissue
XX injury or ischemic injury, including stroke. The compound or composition
XX is also useful for inhibiting the degree or rate of phosphorylation by
XX the protein kinase. The interacting polypeptide or compound is useful in

CC	method of stabilising a hydrophobic pocket- containing protein kinase,
CC	where the protein kinase is exposed to the compound or polypeptide.
CC	AAB99786 to AAB99847 represent amino acid sequences, and AAH44210 and
CC	AAH44211 represent oligonucleotide sequences, used in the exemplification
CC	of the present invention
XX	
XX	Sequence 335 AA;
SO	
Qy	1 ANSFVGTQVYSPELL 16
Db	145 ANSFVGTQVYSPELL 160
RESULT 10	
ID	ADJ38895
XX	ADJ38895 standard; protein; 335 AA.
AC	
XX	ADJ38895;
XX	
DT	06-MAY-2004 (first entry)
XX	
DE	PKX1 amino acid sequence.
XX	
KW	phosphoinositide dependent protein kinase 1; PKX1; molecular modelling;
KW	protein kinase; catalytic domain; enzyme; hydrophobic pocket;
KW	insulin signalling pathway; signalling; crystalline form;
KW	protein co-ordinate data; three-dimensional structure; antifungal;
KW	antidiabetic; cardiant; cycostatic; cerebroprotective; vasotonic;
KW	anorectic; protein kinase modulator; cancer; diabetes; obesity;
KW	apoptosis inhibition; leukaemia disease; stroke; myocardial infarction;
KW	neural injury.
XX	
OS	Unidentified.
XX	
XX	MO2003104481-A2.
PN	
XX	18-DEC-2003.
PD	
XX	09-JUN-2003; 2003MO-GB002509.
PF	
XX	08-JUN-2002; 2002GB-00013186.
PR	
XX	
PA	(UYDU-) UNIV DUNDEE.
PI	Alessi D, Biondi R, Komander D, Van AD;
PI	WPI; 2004-062373/06.
DR	
XX	
XX	
PS	Disclosure; Fig 7; 383pp; English.
CC	The present invention describes a method (M1) for selecting or designing
CC	a compound for modulating the activity of phosphoinositide dependent
CC	protein kinase 1 (PKX1) comprising using molecular modelling means to
CC	select or design a compound that is predicted to interact with the
CC	protein kinase catalytic domain of PKX1, and selecting a compound that is
CC	predicted to interact with the protein kinase catalytic domain. Also
CC	described: (1) selecting or designing (M2) a compound for modulating the
CC	activity of a hydrophobic pocket (PIF binding pocket)-containing protein
CC	kinase having a hydrophobic pocket in the position equivalent to the
CC	hydrophobic pocket of human PKX1 that is defined by residues including
CC	Lys15, Ile18, Ile19, Val124, Val127 and/or Leu155 of full-length human
CC	PKX1 and further having a phosphate binding pocket in the position
CC	equivalent to the phosphate binding pocket of human PKX1 that is defined
CC	by residues including Lys76, Arg131, Thr148 and/or Glu150; (2) assessing
CC	(M3) the activation state of a structure for a protein kinase; (3) a

Query Match	100.0%;	Score 79;	DB 8;	Length 335;
Best Local Similarity	100.0%;	Pred. No. 1,7e-05;		
Matches 16;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0
Qy	1	ANSFVGTAQYVSPDLL 16		
Db	145	ANSFVGTAQYVSPDLL 160		
RESULT 11				
ID	ADY85535			
AC	ADY85535 standard; protein; 361 AA.			
XX	ADY85535;			
XX	16-JUN-2005 (first entry)			
XX	Catalytic domain of PIM kinase-like protein PDPK1.			
XX	Kinase; protein co-ordinate data; protein structure; cancer; cytosolic;			
XX	neoplasm; inflammation; antiinflammatory.			
XX	Unidentified.			
XX	WO2005028624-A2.			
XX	31-MAR-2005.			
XX	15-SEP-2004; 2004WO-US030360.			
XX	15-SEP-2003; 2003US-0503277P.			
XX	(PDEX-) PLEXIKON INC.			
XX	Artis DR, Bremer RE, Gillette SJ, Hurt CR, Ibrahim PL,			
XX	Zuckerman RL;			
XX	WPI; 2005-273155/28.			
XX	New scaffold library used for identifying and developing ligands for			

PT protein kinases and treating kinase associated disorders e.g. cancer,
 PT comprises set of compounds comprising N-heterocyclic compounds.
 XX
 PS Disclosure; Page 175-179; 236pp; English.
 XX
 CC The invention relates to a new kinase scaffold library comprises at least
 CC 1 set of compounds, each set comprising at least 1 N-heterocyclic
 CC compound of formulae (I)-(VII) given in the specification. Also included
 CC are a system for fitting compounds in binding sites of protein kinases
 CC (comprising an electronic kinase scaffold, and a scaffold library
 CC comprising at least 1 collection of electronic representations of (I)-
 CC (VII), where the scaffold library is embedded in a computer device and
 CC the electronic representations of the compounds can be selectively
 CC retrieved and functionally connected with computer software adapted to
 CC fit electronic representations of compounds in an electronic
 CC representation of a binding site of a kinase), obtaining improved ligands
 CC binding to a protein kinase (which comprises determining if a derivative
 CC of (I)-(VII) binds to the kinase with greater affinity and/or specificity
 CC than (I)-(VII)), developing ligands specific for a particular kinase
 CC (which comprises determining if a derivative of (I)-(VII) that binds to
 CC kinases has greater for specificity for the particular kinase than (I)-
 CC (VII)), developing ligands binding to a kinase (which comprises
 CC determining the orientation of at least 1 molecular scaffold of (I)-(VII)
 CC in co-crystals with the kinase, identifying chemical structures of the
 CC scaffold, that, when modified, change the binding affinity and/or
 CC specificity between the scaffold and kinase and synthesizing a ligand in
 CC which at least 1 chemical structure of the scaffold is modified),
 CC developing ligands with increased specificity on a kinase (which
 CC comprises testing a derivative of a kinase binding compound (I)-(VII) for
 CC increased specificity on the kinase), identifying a ligand binding to a
 CC kinase (which comprises determining if a derivative compound including a
 CC core structure (I)-(VII) binds to the kinase with changed binding
 CC affinity and/or specificity), a co-crystal of a kinase and a binding
 CC compound (I)-(VII), preparation of co-crystals of Pim-1 with (I)-(VII),
 CC identifying potential kinase binding compounds (which comprises fitting
 CC electronic representations of (I)-(VII) in an electronic representation
 CC of a kinase binding site), attaching a kinase binding compound to an
 CC attachment component (which comprises identifying energetically allowed
 CC sites for attachment of the compound or derivative to the attachment
 CC (VII) and attaching the compound or derivative to the attachment
 CC component at the allowed site), modified compounds (comprising (I)-(VII))
 CC with an attached linker group, and developing a ligand for a kinase
 CC comprising conserved residues matching at least one of Pim-1 residues 49,
 CC 52, 67, 121, 128 and 186 which comprises determining if (I)-(VII) binds
 CC to the kinase. The kinases comprise Pim-1, Pyk2, c-Adi, Her2, cMet,
 CC vascular endothelial growth factor receptor, endothelial growth factor
 CC receptor, cKit, Pcbeta, p38, Cdk2, Akt or Gsk3beta. The kinase scaffold
 CC library is used for identifying and developing ligands binding to
 CC kinases, for modulating kinase activity and for treating disease
 CC condition associated with abnormal kinase activity e.g. cancer,
 CC inflammatory disease. The method identifies improved ligands binding to a
 CC kinase resulting in ligands having high affinity and specificity towards
 CC kinase. The co-crystals of kinase and the binding compound are of
 CC sufficient size and quality to allow structural determination of at least
 CC 2 Angstroms. The present sequence is a catalytic domain from a Pim-1like
 CC kinase. NOTE: It is not clear whether the sequence as presented
 CC represents a continuous amino acid sequence.
 XX
 SQ Sequence 361 AA;
 QY
 Query Match 100.0%; Score 79; DB 9; Length 361;
 Best Local Similarity 100.0%; Pred. No. 1.8e-05;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 ANSFVGTAGVYSPPELL 16
 |||||
 DB 208 ANSFVGTAGVYSPPELL 223
 RESULT 12
 AEF60044 standard; protein; 462 AA.
 ID AEF60044
 XX

AC AEF60044;
 XX
 DT 06-APR-2006 (first entry)
 XX
 DE Human truncated PDK1.
 XX
 KW kinase; PDK1; protein engineering; enzyme.
 XX
 OS Homo sapiens.
 XX
 FH Key
 FT Misc-difference 3 Location/Qualifiers
 FT Misc-difference 7 /note= "Encoded by CTT"
 FT Misc-difference 7 /note= "Encoded by CTT"
 PD
 XX 02-FEB-2006.
 XX 28-JUL-2005; 2005MO-EP053687.
 PF
 PR 30-JUL-2004; 2004BP-00103693.
 XX
 PA (BYKG) ALTANA PHARMA AG.
 PI Schmidt M, Beckers T;
 XX WPI; 2006-12577/13.
 DR N-PSDB; AEF60043.
 XX
 FT Preparing active kinase containing PH domains, useful for identifying an
 PT Akt1 inhibitor, comprises expressing a derivative of a kinase and
 PT coexpressing a derivative of an activating kinase.
 PS Example 1; Fig 3; 23pp; English.
 XX
 CC The invention relates to a method of preparing an active derivative of a
 CC kinase which, in native form, contains a PH domain, comprises expressing
 CC a derivative of a kinase which, in native form, contains a PH domain, and
 CC coexpressing a derivative of an activating kinase which, in native form,
 CC contains a PH domain, where the derivative of the kinase and the
 CC derivative of the activating kinase do not contain any functional PH
 CC domain. The active Akt derivative is useful for identifying an Akt1
 CC inhibitor. The method is useful for preparing an active derivative of a
 CC kinase, which, in native form, contains a PH domain. The present sequence
 CC represents the amino acid sequence of a human truncated PDK1 which has a
 CC deleted PH domain.
 XX
 SQ Sequence 462 AA;
 QY
 Query Match 100.0%; Score 79; DB 10; Length 462;
 Best Local Similarity 100.0%; Pred. No. 2.4e-05;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 ANSFVGTAGVYSPPELL 16
 |||||
 DB 251 ANSFVGTAGVYSPPELL 266
 RESULT 13
 ABU04719 standard; protein; 468 AA.
 ID ABU04719
 XX
 AC ABU04719;
 XX
 DT 29-JAN-2003 (first entry)
 XX
 DE Human expressed protein tag (EPT) #1385.
 XX
 KM Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
 KM protease; protease inhibitor; transporter; cytoskeletal protein;

KM receptor; transcription factor; cancer; MHC;
 KM major histocompatibility complex; myeloma; colon cancer; gastric cancer;
 KM adenocarcinoma; sarcoma; melanoma; lymphoma; leukemia.
 XX
 OS Homo sapiens.
 XX
 PN WO200278524-A2.
 XX
 PD 10-OCT-2002.
 XX
 PF 28-MAR-2002; 2002WO-US009671.
 XX
 PR 28-MAR-2001; 2001US-0279495P.
 XX
 PR 21-MAY-2001; 2001US-0292544P.
 PR 08-AUG-2001; 2001US-0310801P.
 PR 01-OCT-2001; 2001US-0326370P.
 PR 04-DEC-2001; 2001US-0336780P.
 PR 20-FEB-2002; 2002US-0358985P.
 XX
 PA (ZYCO-) ZYCOS INC.
 XX
 PI Chicx RM, Tomlinson AJ, Urban RG;
 XX
 DR WPI; 2003-040607/03.
 XX
 PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
 PT cytoskeletal proteins, receptors or transcription factors), useful for
 PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
 PT leukemia.
 XX
 PS Example 2; SEQ ID NO 1385; 134pp; English.
 XX
 CC The invention describes a purified polypeptide, which comprises a
 CC fragment of a kinase, phosphatase, protease, protease inhibitor,
 CC transporter, cytoskeletal protein, receptor or transcription factor. The
 CC polypeptide is useful as an immunogenic composition for eliciting in a
 CC mammal an immunogenic response directed against any of the purified
 CC polypeptide. The purified polypeptide, or the antibody that binds to this
 CC polypeptide, is useful for treating cancer. The polypeptide is also
 CC useful for identifying compounds that binds to a naturally processed
 CC class I or class II MHC-binding polypeptide. The polypeptides and
 CC polynucleotides are particularly useful for treating or preventing
 CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
 CC lymphoma or leukemia. These are also useful for screening agents for
 CC treating the above mentioned diseases. This sequence represents an
 CC expressed protein tag (EPT) isolated from human tissue for translational
 CC profiling. Note: This sequence does not appear in the printed
 CC specification but was obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 468 AA:
 Query Match 100.0%; Score 79; DB 6; Length 468;
 Best Local Similarity 100.0%; Pred. No. 2,4e-05;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ANSFVGTAAQYVSPPELL 16
 Db 151 ANSFVGTAAQYVSPPELL 166
 RESULT 14
 ID ABOU4705 standard; protein; 468 AA.
 XX
 AC ABOU4705;
 XX
 DT 29-JAN-2003 (first entry)
 XX
 DE Human expressed protein tag (EPT) #1371.
 XX
 KM Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
 KM protease; protease inhibitor; transporter; cytoskeletal protein;

KM receptor; transcription factor; cancer; MHC;
 KM major histocompatibility complex; myeloma; colon cancer; gastric cancer;
 KM adenocarcinoma; sarcoma; melanoma; lymphoma; leukemia.
 XX
 OS Homo sapiens.
 XX
 PN WO200278524-A2.
 XX
 PD 10-OCT-2002.
 XX
 PF 28-MAR-2002; 2002WO-US009671.
 XX
 PR 28-MAR-2001; 2001US-0279495P.
 XX
 PR 21-MAY-2001; 2001US-0292544P.
 PR 08-AUG-2001; 2001US-0310801P.
 PR 01-OCT-2001; 2001US-0326370P.
 PR 04-DEC-2001; 2001US-0336780P.
 PR 20-FEB-2002; 2002US-0358985P.
 XX
 PA (ZYCO-) ZYCOS INC.
 XX
 PI Chicx RM, Tomlinson AJ, Urban RG;
 XX
 DR WPI; 2003-040607/03.
 XX
 PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
 PT cytoskeletal proteins, receptors or transcription factors), useful for
 PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
 PT leukemia.
 XX
 PS Example 2; SEQ ID NO 1371; 134pp; English.
 XX
 CC The invention describes a purified polypeptide, which comprises a
 CC fragment of a kinase, phosphatase, protease, protease inhibitor,
 CC transporter, cytoskeletal protein, receptor or transcription factor. The
 CC polypeptide is useful as an immunogenic composition for eliciting in a
 CC mammal an immunogenic response directed against any of the purified
 CC polypeptide. The purified polypeptide, or the antibody that binds to this
 CC polypeptide, is useful for treating cancer. The polypeptide is also
 CC useful for identifying compounds that binds to a naturally processed
 CC class I or class II MHC-binding polypeptide. The polypeptides and
 CC polynucleotides are particularly useful for treating or preventing
 CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
 CC lymphoma or leukemia. These are also useful for screening agents for
 CC treating the above mentioned diseases. This sequence represents an
 CC expressed protein tag (EPT) isolated from human tissue for translational
 CC profiling. Note: This sequence does not appear in the printed
 CC specification but was obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 468 AA:
 Query Match 100.0%; Score 79; DB 6; Length 468;
 Best Local Similarity 100.0%; Pred. No. 2,4e-05;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ANSFVGTAAQYVSPPELL 16
 Db 151 ANSFVGTAAQYVSPPELL 166
 RESULT 15
 ID AAY05780 standard; protein; 506 AA.
 XX
 AC AAY05780;
 XX
 DT 02-AUG-1999 (first entry)
 XX
 DE Human protein kinase B kinase.
 XX
 KM Protein kinase B kinase; PKB kinase; inhibitor; assay; cytostatic;
 KM cell proliferation; cancer; therapy; signal transduction; human.


```

XX OS Homo sapiens.
XX
XX Key Location/Qualifiers
XX FT Domain 31..303
XX FT /note="protein kinase domain"
XX FT 367..494
XX FT /note="pH domain"
XX
XX MO991687-A2.
XX
XX 08-APR-1999.
XX
XX 17-SEP-1998; 98MO-US019412.
XX
XX 26-SEP-1997; 97US-0060190P.
XX
XX (ONYX-) ONYX PHARM INC.
XX
XX Stephens L, Hawkins P, Stokoe D;
XX WPI; 1999-263699/22.
XX DR N-PSDB; AAX25486.
XX
XX PT Protein kinase B kinase nucleotide sequence and product.
XX
XX Example 1; Fig 3; 38pp; English.
XX
XX The present sequence represents a 55 kDa protein kinase B (PKB) kinase
XX CC that activates PKB in the signal transduction pathway of
XX CC phosphatidylinositol-3,4,5-trisphosphate (PIP3). The sequence is
XX CC predicted from EST clones and cDNAs isolated from a human U937 cell
XX CC library. The following are claimed: (1) an isolated nucleic acid molecule
XX CC containing a nucleotide sequence which encodes PKB kinase activity; (2) a
XX CC nucleotide sequence encoding a chimeric protein comprising the nucleic
XX CC acid molecule fused to a second nucleotide sequence encoding a
XX CC heterologous protein; (3) an expression vector; (4) a host cell; (5) an
XX CC antibody that immunospecifically binds to PKB kinase; (6) a method for
XX CC diagnosing disease in a mammal by detecting a PKB kinase gene mutation in
XX CC the mammal's genome; (7) a method for screening compounds for treatment
XX CC of cell growth disorders utilizing activated PKB kinase; (8) activation
XX CC of PKB kinase by incubation in solution with PIP3; (9) compounds
XX CC identified in (7); and (10) an isolated PKB kinase. PKB is involved in
XX CC regulating cell growth, hence PKB kinase inhibitors can be used to treat
XX CC disease involving unwanted cell growth, including cancer.
XX
XX SQ Sequence 506 AA;
XX
XX Query Match 100.0%; Score 79; DB 2; Length 506;
XX Best Local Similarity 100.0%; Pred. No. 2.7e-05;
XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 ANSFVGTAGYVSPELL 16
XX | | | | | | | | | | | | | | | |
XX DB 189 ANSFVGTAGYVSPELL 204
XX
XX RESULT 16
XX ABBU04715
XX ID ABBU04715 standard; protein; 506 AA.
XX
XX AC ABBU04715;
XX
XX DT 29-JAN-2003 (first entry)
XX
XX DE Human expressed protein tag (EPT) #1381.
XX
XX KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
XX KW protease; protease inhibitor; transporter; cytoskeletal protein;
XX KW receptor; transcription factor; cancer; MHC;
XX KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
XX KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukemia.
XX
XX

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OS OS Homo sapiens.
XX
XX FN MO200278524-A2.
XX
XX PD 10-OCT-2002.
XX
XX FE 28-MAR-2002; 2002MO-US009671.
XX
XX 28-MAR-2001; 2001US-0279495P.
XX 21-MAY-2001; 2001US-0292544P.
XX 08-AUG-2001; 2001US-0310801P.
XX 01-OCT-2001; 2001US-0326370P.
XX 04-DEC-2001; 2001US-0336780P.
XX 20-FEB-2002; 2002US-0358985P.
XX
XX (ZYCO-) ZYCO INC.
XX
XX Chicx RM, Tomlinson AJ, Urban RG;
XX WPI; 2003-040607/03.
XX
XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
XX PT cytoskeletal proteins, receptors or transcription factors), useful for
XX PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
XX PT leukemia.
XX
XX Example 2; SEQ ID NO 1381; 134pp; English.
XX
XX PS The invention describes a purified polypeptide, which comprises a
XX CC fragment of a kinase, phosphatase, protease, protease inhibitor,
XX CC transporter, cytoskeletal protein, receptor or transcription factor. The
XX CC polypeptide is useful as an immunogenic composition for eliciting in a
XX CC mammal an immunogenic response directed against any of the purified
XX CC polypeptide. The purified polypeptide, or the antibody that binds to this
XX CC polypeptide, is useful for treating cancer. The polypeptide is also
XX CC useful for identifying compounds that binds to a naturally processed
XX CC class I or class II MHC-binding polypeptide. The polypeptides and
XX CC polynucleotides are particularly useful for treating or preventing
XX CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
XX CC lymphoma or leukaemia. These are also useful for screening agents for
XX CC treating the above mentioned diseases. This sequence represents an
XX CC expressed protein tag (EPT) isolated from human tissue for translational
XX CC profiling. Note: This sequence does not appear in the printed
XX CC specification but was obtained in electronic format directly from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 506 AA;
XX
XX Query Match 100.0%; Score 79; DB 6; Length 506;
XX Best Local Similarity 100.0%; Pred. No. 2.7e-05;
XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 ANSFVGTAGYVSPELL 16
XX | | | | | | | | | | | | | | | |
XX DB 189 ANSFVGTAGYVSPELL 204
XX
XX RESULT 17
XX AAB99823
XX ID AAB99823 standard; protein; 535 AA.
XX
XX AC AAB99823;
XX
XX DT 20-SEP-2001 (first entry)
XX
XX DE AGC protein kinase family member PDK1 protein sequence.
XX
XX KW Protein kinase, identification; hydrophobic pocket; interacting; cancer;
XX KW diabetes; inhibition; apoptosis; tissue injury; ischemic injury; stroke.
XX
XX OS Homo sapiens.
XX OS Synthetic.
XX

```

PN WO200144497-A2.
 XX
 PD 21-JUN-2001.
 XX
 XX 04-DEC-2000; 2000WO-GB004598.
 PF
 XX 02-DEC-1999; 99US-0168559P.
 PR
 XX (UYDU-) UNIV DUNDEE.
 PA
 XX Aleesi D, Biondi R;
 PI WPI; 2001-390252/41.
 DR
 XX Identifying modulators of protein kinase (PK) activity, useful in
 PT developing drugs for treating cancer or diabetes, by measuring the
 PT ability of the compound to modulate or mimic the interaction of PK with
 PT interacting polypeptides.
 PS Disclosure; Fig 15; 180pp; English.
 XX
 CC The present invention describes a method for identifying a compound that
 CC modulates protein kinase activity. The method comprises measuring the
 CC ability of the compound to inhibit, promote or mimic the interaction of a
 CC hydrophobic pocket-containing protein kinase with an interacting
 CC polypeptide. The interacting polypeptide interacts with the hydrophobic
 CC pocket of the protein kinase and/or comprises the amino acid sequence
 CC Phe/Tyr-Xaa-Xaa-Phe/Tyr (1). The method is useful in screening assays for
 CC developing pharmaceutical compounds or drugs. Compounds, polypeptides or
 CC polynucleotides from the present invention are useful in medicine,
 CC particularly in the manufacture of a medicament for treating a patient in
 CC need of modulation of signalling by a hydrophobic pocket-containing
 CC protein kinase. Specifically, the patient has cancer or diabetes or is in
 CC need of inhibition of apoptosis, e.g. a patient suffering from tissue
 CC injury or ischaemic injury, including stroke. The compound or composition
 CC is also useful for inhibiting the degree or rate of phosphorylation by
 CC the protein kinase. The interacting polypeptide or compound is useful in
 CC methods of stabilising a hydrophobic pocket-containing protein kinase,
 CC where the protein kinase is exposed to the compound or polypeptide.
 CC AAB9786 to AAB99847 represent amino acid sequences, and AA44410 and
 CC AA44411 represent oligonucleotide sequences, used in the exemplification
 CC of the present invention
 CC
 XX
 SQ Sequence 535 AA:
 Query Match 100.0%; Score 79; DB 4; Length 535;
 Best Local Similarity 100.0%; Pred. No. 2,9e-05;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ANSFVGTAGYVSPPELL 16
 Db 218 ANSFVGTAGYVSPPELL 233
 RESULT 18
 ABU04713
 ID ABU04713 standard; protein; 535 AA.
 XX
 AC ABU04713;
 XX
 DT 29-JAN-2003 (first entry)
 XX
 DE Human expressed protein tag (EPT) #1379.
 XX
 KM Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
 KM protease; protease inhibitor; transporter; cytoskeletal protein;
 KM receptor; transcription factor; cancer; MHC;
 KM major histocompatibility complex; myeloma; colon cancer; gastric cancer;
 KM adenocarcinoma; sarcoma; melanoma; lymphoma; leukemia.
 XX
 OS Homo sapiens.
 XX
 XX WO200278524-A2.
 PN

XX
 PD 10-OCT-2002.
 XX
 XX 26-MAR-2002; 2002WO-US009671.
 PF
 XX 28-MAR-2001; 2001US-0279495P.
 PR 21-MAY-2001; 2001US-0292544P.
 PR 08-AUG-2001; 2001US-0310801P.
 PR 01-OCT-2001; 2001US-0326370P.
 PR 04-DEC-2001; 2001US-0336780P.
 PR 20-FEB-2002; 2002US-0358985P.
 XX
 XX (ZYCO-) ZYCO INC.
 PA
 XX Chicz RM, Tomlinson AJ, Urban RG;
 PI WPI; 2003-040607/03.
 DR
 XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
 PT cytoskeletal proteins, receptors or transcription factors), useful for
 PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
 PT leukemia.
 XX
 XX Example 2; SEQ ID NO 1379; 134pp; English.
 PS
 XX The invention describes a purified polypeptide, which comprises a
 CC fragment of a kinase, phosphatase, protease, protease inhibitor,
 CC transporter, cytoskeletal protein, receptor or transcription factor. The
 CC polypeptide is useful as an immunogenic composition for eliciting in a
 CC mammal an immunogenic response directed against any of the purified
 CC polypeptide. The purified polypeptide, or the antibody that binds to this
 CC polypeptide, is useful for treating cancer. The polypeptide is also
 CC useful for identifying compounds that binds to a naturally processed
 CC class I or class II MHC-binding polypeptide. The polypeptides and
 CC polynucleotides are particularly useful for treating or preventing
 CC lymphoma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
 CC myeloma or leukemia. These are also useful for screening agents for
 CC treating the above mentioned diseases. This sequence represents an
 CC expressed protein tag (EPT) isolated from human tissue for translational
 CC profiling. Note: This sequence does not appear in the printed
 CC specification but was obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 CC
 XX
 SQ Sequence 535 AA:
 Query Match 100.0%; Score 79; DB 6; Length 535;
 Best Local Similarity 100.0%; Pred. No. 2,9e-05;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ANSFVGTAGYVSPPELL 16
 Db 218 ANSFVGTAGYVSPPELL 233
 RESULT 19
 AAW71738
 ID AAW71738 standard; protein; 556 AA.
 XX
 AC AAW71738;
 XX
 DT 10-DEC-1998 (first entry)
 XX
 DE Human 3-phosphoinositide-dependent protein kinase.
 XX
 KM Protein kinase B-alpha; 3-phosphoinositide-dependent protein kinase;
 KM diabetes; cancer; cell proliferation; phosphorylation.
 KM
 OS Homo sapiens.
 XX
 XX WO9841638-A1.
 PN
 XX 24-SEP-1998.
 PD
 XX

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PF 16-MAR-1998; 98WO-GB000777.
XX
XX 17-MAR-1997; 97GB-00005462.
PR 19-JUN-1997; 97GB-00012826.
PR 15-AUG-1997; 97GB-00017253.
PR 03-OCT-1997; 97US-00943667.
XX
XX (MEDI-) MEDICAL RES COUNCIL.
XX
XX Alessi DR;
XX
XX MPI; 1998-531572/45.
DR N-PSDB; AAV61037.
XX
XX New isolated 3-phosphoinositide-dependent protein kinase - which
PT phosphorylates and activates protein kinase B-alpha, used to develop
PT products for treating diabetes or cancers or for enhancing cell
PT proliferation.
XX
XX Example 2; Fig 10; 120pp; English.
XX
XX A pure 3-phosphoinositide-dependent protein kinase (3PDK) that
CC phosphorylates and activates PK B-alpha has been isolated. The present
CC sequence represents human 3PDK. Products from the present invention
CC (e.g. 3PDK, nucleotide sequence encoding 3PDK, antibodies against
CC 3PDK) can be used to identify compounds which modulate the PK activity
CC e.g. for treating diabetes or cancers or for enhancing cell proliferation
CC in the regeneration of nerves or in wound healing
XX
XX Sequence 556 AA;
SQ
Query Match 100.0%; Score 79; DB 2; Length 556;
Best Local Similarity 100.0%; Pred. No. 3e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 ANSFVGTAGVSPBL 16
DB 239 ANSFVGTAGVSPBL 254
RESULT 20
AA27055
ID AA27055 standard; protein; 556 AA.
XX
XX AA27055;
XX
XX 08-OCT-1999 (first entry)
XX
XX Human protein kinase (HPKM)-4 (clone ID 472480).
XX
XX Human protein kinase molecule; HPKM; human; protein kinase;
XX phosphate group; cancer; immune disorder.
XX
XX Homo sapiens.
XX
XX WO9938981-A2.
XX
XX 05-AUG-1999.
XX
XX 12-JAN-1999; 99WO-US0000661.
XX
XX 30-JAN-1998; 98US-00016000.
XX
XX (INCY-) INCYTE PHARM INC.
XX
XX Bandman O, Hillman JL, Lal P, Akerblom IE, Shah P, Corley NC;
PI Guejter KJ;
XX
XX MPI; 1999-479190/40.
DR N-PSDB; AAX89853.
XX
XX New human protein kinase molecules useful for treating or preventing
PT cancer or an immune disorder.

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XX
XX Claim 1; Page 68-69; 77pp; English.
XX
XX The invention provides human protein kinase molecules (HPKM) (AA27052-
CC 57) and nucleic acid sequences (AAX89850-55) encoding the HPKM
CC polypeptides respectively. The HPKM polypeptides can be produced
CC recombinantly by standard recombinant methodology. Protein kinases add
CC phosphate groups to proteins. HPKM polypeptide or an HPKM antagonist is
CC used to treat or prevent cancer or an immune disorder. The present
CC sequence represents the amino acid sequence of HPKM-4
XX
XX Sequence 556 AA;
SQ
Query Match 100.0%; Score 79; DB 2; Length 556;
Best Local Similarity 100.0%; Pred. No. 3e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 ANSFVGTAGVSPBL 16
DB 239 ANSFVGTAGVSPBL 254
RESULT 21
AA27055
ID AA27055 standard; protein; 556 AA.
XX
XX AA27055;
XX
XX 17-OCT-2003 (revised)
XX
XX 02-AUG-1999 (first entry)
XX
XX Human protein kinase B kinase.
XX
XX Protein kinase B kinase; PKB kinase; inhibitor; assay; cytostatic;
XX cell proliferation; cancer; therapy; signal transduction; human; rat.
XX
XX Homo sapiens.
XX
XX Rattus sp.
XX
XX Chimeric.
XX
XX Key Location/Qualifiers
XX FH 1..13
XX FT /note= "rat-derived sequence"
XX FT Misc-difference 60
XX FT /note= "encoded by CCM"
XX FT Domain 72..353
XX FT /note= "protein kinase domain"
XX FT Domain 417..544
XX FT /note= "PH domain"
XX
XX WO9916887-A2.
XX
XX 08-APR-1999.
XX
XX 17-SEP-1998; 98WO-US019412.
XX
XX 26-SEP-1997; 97US-0060190P.
XX
XX (ONYX-) ONYX PHARM INC.
XX
XX Stephens L, Hawkins P, Stokoe D;
PI MPI; 1999-263699/22.
DR N-PSDB; AAX25486.
XX
XX Protein kinase B kinase nucleotide sequence and product.
XX
XX Claim 1; Fig 5; 38pp; English.
XX
XX The present sequence represents a protein kinase B (PKB) kinase that
CC activates PKB in the signal transduction pathway of phosphatidylinositol-
CC 3,4,5-trisphosphate (PIP3). The sequence is predicted from EST clones and
CC cDNAs isolated from a human U937 cell library and from a clone obtained

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CC from a rat brain cDNA library. The following are claimed: (1) an isolated
CC nucleic acid molecule containing a nucleotide sequence which encodes PKB
CC kinase activity; (2) a nucleotide sequence encoding a chimeric protein
CC comprising the nucleic acid molecule fused to a second nucleotide
CC sequence encoding a heterologous protein; (3) an expression vector; (4) a
CC host cell; (5) an antibody that immunospecifically binds to PKB kinase;
CC (6) a method for diagnosing disease in a mammal by detecting a PKB kinase
CC gene mutation in the mammal's genome; (7) a method for screening
CC compounds for treatment of cell growth disorders utilizing activated PKB
CC kinase; (8) activation of PKB kinase by incubation in solution with PIP₃;
CC (9) compounds identified in (7); and (10) an isolated PKB kinase. PKB is
CC involved in regulating cell growth, hence PKB kinase inhibitors can be
CC used to treat disease involving unwanted cell growth, including cancer.
CC (Updated on 17-OCT-2003 to standardise OS field)

CC XX Sequence 556 AA;

CC SQ

CC Query Match 100.0%; Score 79; DB 2; Length 556;
CC Best Local Similarity 100.0%; Pred. No. 3e-05;
CC Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC QY 1 ANSFVGTAGYVSPDLL 16
CC |||||
CC Db 239 ANSFVGTAGYVSPDLL 254

CC RESULT 22

CC AAB28445
CC ID AAB28445 standard; protein; 556 AA.

CC XX AAB28445;

CC AC

CC XX 01-FEB-2001 (first entry)

CC DT

CC XX Human PDK-1.

CC DE

CC XX Human; PDK-1; 3-phosphoinositide dependent protein kinase-1;
CC KM antisense oligonucleotide; phosphorothioate; antiinflammatory;
CC KM cytosratic; antimicrobial.

CC XX

CC OS Homo sapiens.

CC OS US6124272-A.

CC PN

CC XX 26-SEP-2000.

CC PD

CC XX 09-APR-1999; 99US-00289466.

CC PF

CC XX 09-APR-1999; 99US-00289466.

CC PR

CC XX 09-APR-1999; 99US-00289466.

CC XX

CC PA (ISIS-) ISIS PHARM INC.

CC XX

CC XX Monia BP, Cowseert LM;

CC PI

CC XX WPI; 2000-611015/58.

CC DR

CC XX N-PSDB; AAC60590.

CC DR

CC XX Novel antisense compounds useful for inhibiting the expression of human 3
CC PT -phosphoinositide dependent protein kinase-1, useful e.g. for treating
CC PT inflammation, tumors and infections.

CC XX

CC PS Disclousure; Col 45-48; 41pp; English.

CC XX

CC The nucleotide sequence encoding the present protein was used to design a
CC large number of antisense oligonucleotides which are targeted to a
CC nucleic acid molecule encoding human 3-phosphoinositide dependent protein
CC kinase-1 (PDK-1). The antisense compounds may be oligodeoxynucleotides or
CC chimeric oligonucleotides containing a central gap region, consisting of
CC ten 2'-deoxynucleotides, which is flanked on both sides by 2'-
CC methoxyethyl (2'-MOE) wings. The oligonucleotides have a phosphorothioate
CC backbone. The antisense oligonucleotides are useful for inhibiting the
CC expression of human PDK-1 in human cells or tissues. They are also useful
CC for preventing or delaying infection, inflammation or tumours and are

CC useful for research and diagnostics

CC XX

CC SQ Sequence 556 AA;

CC Query Match 100.0%; Score 79; DB 3; Length 556;
CC Best Local Similarity 100.0%; Pred. No. 3e-05;
CC Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC QY 1 ANSFVGTAGYVSPDLL 16
CC |||||
CC Db 239 ANSFVGTAGYVSPDLL 254

CC RESULT 23

CC AAB28446
CC ID AAB28446 standard; protein; 556 AA.

CC XX AAB28446;

CC AC

CC XX 01-FEB-2001 (first entry)

CC DT

CC XX Human PDK-1.

CC DE

CC XX Human; PDK-1; 3-phosphoinositide dependent protein kinase-1;
CC KM antisense oligonucleotide; phosphorothioate; antiinflammatory;
CC KM cytosratic; antimicrobial.

CC XX

CC OS Homo sapiens.

CC OS US6124272-A.

CC PN

CC XX 26-SEP-2000.

CC PD

CC XX 09-APR-1999; 99US-00289466.

CC PF

CC XX 09-APR-1999; 99US-00289466.

CC PR

CC XX 09-APR-1999; 99US-00289466.

CC XX

CC PA (ISIS-) ISIS PHARM INC.

CC XX

CC XX Monia BP, Cowseert LM;

CC PI

CC XX WPI; 2000-611015/58.

CC DR

CC XX N-PSDB; AAC60591.

CC DR

CC XX Novel antisense compounds useful for inhibiting the expression of human 3
CC PT -phosphoinositide dependent protein kinase-1, useful e.g. for treating
CC PT inflammation, tumors and infections.

CC XX

CC PS Disclousure; Col 49-52; 41pp; English.

CC XX

CC The nucleotide sequence encoding the present protein was used to design a
CC large number of antisense oligonucleotides which are targeted to a
CC nucleic acid molecule encoding human 3-phosphoinositide dependent protein
CC kinase-1 (PDK-1). The antisense compounds may be oligodeoxynucleotides or
CC chimeric oligonucleotides containing a central gap region, consisting of
CC ten 2'-deoxynucleotides, which is flanked on both sides by 2'-
CC methoxyethyl (2'-MOE) wings. The oligonucleotides have a phosphorothioate
CC backbone. The antisense oligonucleotides are useful for inhibiting the
CC expression of human PDK-1 in human cells or tissues. They are also useful
CC for preventing or delaying infection, inflammation or tumours and are
CC useful for research and diagnostics

CC XX

CC SQ Sequence 556 AA;

CC Query Match 100.0%; Score 79; DB 3; Length 556;
CC Best Local Similarity 100.0%; Pred. No. 3e-05;
CC Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC QY 1 ANSFVGTAGYVSPDLL 16
CC |||||
CC Db 239 ANSFVGTAGYVSPDLL 254

RESULT 24
 ID AAY94735 standard; protein; 556 AA.
 AC AAY94735;
 XX
 DT 29-JAN-2001 (first entry)
 XX
 DE Phosphoinositide dependent protein kinase 1 (PDK1).
 XX
 KW Substrate specificity; phosphoinositide-dependent protein kinase 1; PDK1;
 KW protein kinase C related protein kinase 2; PRK2; cancer; apoptosis;
 KW mechanical tissue damage; ischaemic disease; stroke;
 KW myocardial infarction; antigenic peptide.
 OS Unidentified.
 XX
 PN MO200056864-A2.
 XX
 PD 28-SEP-2000.
 XX
 PF 17-MAR-2000; 2000WO-GB001004.
 XX
 PR 19-MAR-1999; 99GB-00006245.
 PA (UTDU-) UNIV DUNDEE.
 PI Alessi D, Balendran A, Deak M, Currie R, Downes P, Casamayor A;
 XX
 DR WPI; 2000-647155/62.
 XX
 PT Altering substrate specificity of phosphoinositide-dependent protein
 PT kinase 1, to phosphorylate Ser473 in addition to Thr308 by exposing to
 PT interacting polypeptide.
 XX
 PS Disclosure: Fig 10; 103pp; English.
 XX
 CC This invention relates to a method for altering the substrate specificity
 CC of phosphoinositide-dependent protein kinase 1 (PDK1), by exposing it to
 CC an interacting polypeptide. Included in the invention are a preparation
 CC comprising PDK1 and an interacting polypeptide, PDK1 with altered
 CC specificity is useful for phosphorylating a residue corresponding to the
 CC Ser/Thr residue of a substrate with the following peptide Phe/Tyr-Xaa-Xaa
 CC -Phe/Tyr-Ser/Thr-Phe/Tyr. Altered PDK1 is also used for phosphorylating
 CC protein kinase C related protein kinase 2 (PRK2). The compound identified
 CC by method of the invention that are capable of altering the substrate
 CC specificity of PDK1 are useful for manufacturing a medicament for
 CC treating a patient who is in need of modulation of the insulin signalling
 CC pathway and/or PDK1, PDK2 or PRK2 signalling. A compound that is capable
 CC of reducing the activity (i.e. the PDK1 and/or the PDK2 activity) of PDK1
 CC may be useful in treating cancer. PDK1, e.g. via protein kinase B and/or
 CC SGK, may be capable of providing a survival signal that protects cells
 CC from apoptosis induced in a variety of ways. Reduction of the activity of
 CC PDK1 may promote apoptosis and may be useful in treating cancer.
 CC Conditions in which aiding apoptosis may be benefit may also include
 CC resolution of inflammation. A compound capable of increasing the activity
 CC of PDK1 may be useful in treating diabetes or obesity, or may be useful
 CC in inhibiting apoptosis. Increased activity of PDK1 may lead to increased
 CC levels of leptin, which may lead to weight loss. The compounds may
 CC suppress apoptosis, which may aid cell survival during or following cell
 CC damaging processes and in treating disease in which apoptosis is
 CC involved. Examples of the diseases include, mechanical (including heart)
 CC tissue injury or ischaemic disease, for example stroke and myocardial
 CC infarction, or neural injury. The present sequence represents a
 CC phosphoinositide-dependent-protein kinase 1 amino acid sequence
 XX
 SQ Sequence 556 AA;
 Query Match 100.0%; Score 79; DB 3; Length 556;
 Best Local Similarity 100.0%; Pred. No. 3e-05;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 ANSFVGTNRQYVSPRL 16

DB 239 ANSFVGTNRQYVSPRL 254
 |||||
 RESULT 25
 ID ABO07176 standard; protein; 556 AA.
 AC ABO07176;
 XX
 DT 13-AUG-2003 (first entry)
 XX
 DE Human p53 modifying protein, SEQ ID 136.
 XX
 KW Human; p53 modifier; cytoskeletal; cancer; cytostatic; antiangiogenic;
 KW antiapoptotic; p53 pathway; breast cancer; colon cancer; kidney cancer;
 KW lung cancer; ovarian cancer; angiogenesis; cell cycle;
 KW apoptotic disorder; cell proliferation disorder.
 XX
 OS Homo sapiens.
 XX
 PN MO200299122-A1.
 XX
 PD 12-DEC-2002.
 XX
 PF 03-JUN-2002; 2002WO-US017382.
 XX
 PR 05-JUN-2001; 2001US-0296076P.
 PR 10-OCT-2001; 2001US-0328605P.
 PR 15-FEB-2002; 2002US-0357253P.
 PA (EXEL-) EXELIXIS INC.
 PI Friedman L, Plowman GD, Belvin M, Francis-Lang H, Li D, Funke RP;
 XX
 DR WPI; 2003-156859/15.
 DR N-PSDB; ACD13352.
 XX
 PT Identifying modulators of the p53 pathway for use in treating apoptotic
 PT or cell proliferation disorders, comprises screening for agents that
 PT modulate activity of a human ortholog of genes that modify the p53
 PT pathway in Drosophila.
 XX
 PS Example 2; Page 439-440; 678pp; English.
 XX
 CC The invention relates to identifying (M1) a candidate p53 pathway
 CC modulating agent, by contacting an assay system comprising a purified HM
 CC polypeptide (human ortholog of genes that modify the p53 pathway in
 CC Drosophila) or nucleic acid with a test agent under conditions, where but
 CC for the presence of the test agent, the system provides a reference
 CC activity, and detecting a test agent-biased activity of the assay system.
 CC Also included are modulating (M2) a p53 pathway of a cell (comprising
 CC contacting a cell defective in p53 function with a candidate modulator
 CC that specifically binds to a HM polypeptide comprising an HM amino acid
 CC sequence, where p53 function is restored), modulating (M3) a p53 pathway
 CC in a mammalian cell (comprising contacting the cell with an agent that
 CC specifically binds an HM polypeptide or nucleic acid) and diagnosing (M4)
 CC a disease in a patient (comprising: (a) obtaining a biological sample
 CC from the patient; (b) contacting the sample with a probe for HM
 CC expression; (c) comparing the results with a control; and (d) determining
 CC whether the comparison indicates a likelihood disease). (M1) is useful
 CC for identifying modulators of the p53 pathway. A probe for HM expression
 CC is useful for diagnosing breast, colon, kidney, lung and ovarian cancer,
 CC in a patient, where the cancer has greater than 25 % expression level.
 CC Modulators identified by (M1) are useful in a variety of diagnostic and
 CC therapeutic applications, where disease or disorder prognosis is related
 CC to defects in the p53 pathway, such as, angiogenesis, apoptotic or cell
 CC proliferation disorders (e.g. cancer). Another two new methods (M2 and
 CC M3) are useful for modulating the p53 pathway of a cell, thus restoring
 CC the p53 function of the cell, so that the cell undergoes normal
 CC proliferation or progression through the cell cycle. (M2) and (M3) are
 CC also useful for treating defects in the p53 pathway such as angiogenic,
 CC apoptotic or cell proliferation disorders. The present sequence

CC represents a human p53 pathway modifying protein
XX
SQ Sequence 556 AA;

Query Match 100.0%; Score 79; DB 6; Length 556;
Best Local Similarity 100.0%; Pred. No. 3e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ANSFVGTAGYVSPDLL 16
| | | | | | | | | | | | | | | | | | | | | |
Db 239 ANSFVGTAGYVSPDLL 254

RESULT 26

ABU04708
ID ABU04708 standard; protein; 556 AA.

XX
AC ABU04708;

XX
DT 29-JAN-2003 (first entry)

XX
DE Human expressed protein tag (EPT) #1374.

XX
KM Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KM protease; protease inhibitor; transporter; cytoskeletal protein;
KM receptor; transcription factor; cancer; MHC;
KM major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KM adenocarcinoma; sarcoma; melanoma; lymphoma; leukemia.

XX
OS Homo sapiens.

XX
PN W0200278524-A2.

XX
PD 10-OCT-2002.

XX
PF 28-MAR-2002; 2002WO-US009671.

XX
PR 28-MAR-2001; 2001US-0279495P.

XX
PR 21-MAY-2001; 2001US-0292544P.

XX
PR 08-AUG-2001; 2001US-0310801P.

XX
PR 01-OCT-2001; 2001US-0326370P.

XX
PR 04-DEC-2001; 2001US-0336780P.

XX
PR 20-FEB-2002; 2002US-0358985P.

XX
PA (ZYCO-) ZYCOS INC.

XX
PI Chicz RM, Tomlinson AJ, Urban RG;

XX
DR WPI; 2003-040607/03.

XX
PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.

XX
PS Example 2; SEQ ID NO 1374; 134pp; English.

XX
CC The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at

CC fcp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 556 AA;

Query Match 100.0%; Score 79; DB 6; Length 556;
Best Local Similarity 100.0%; Pred. No. 3e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ANSFVGTAGYVSPDLL 16
| | | | | | | | | | | | | | | | | | | | | |
Db 239 ANSFVGTAGYVSPDLL 254

RESULT 27

ABU04718
ID ABU04718 standard; protein; 556 AA.

XX
AC ABU04718;

XX
DT 29-JAN-2003 (first entry)

XX
DE Human expressed protein tag (EPT) #1384.

XX
KM Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KM protease; protease inhibitor; transporter; cytoskeletal protein;
KM receptor; transcription factor; cancer; MHC;
KM major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KM adenocarcinoma; sarcoma; melanoma; lymphoma; leukemia.

XX
OS Homo sapiens.

XX
PN W0200278524-A2.

XX
PD 10-OCT-2002.

XX
PF 28-MAR-2002; 2002WO-US009671.

XX
PR 28-MAR-2001; 2001US-0279495P.

XX
PR 21-MAY-2001; 2001US-0292544P.

XX
PR 08-AUG-2001; 2001US-0310801P.

XX
PR 01-OCT-2001; 2001US-0326370P.

XX
PR 04-DEC-2001; 2001US-0336780P.

XX
PR 20-FEB-2002; 2002US-0358985P.

XX
PA (ZYCO-) ZYCOS INC.

XX
PI Chicz RM, Tomlinson AJ, Urban RG;

XX
DR WPI; 2003-040607/03.

XX
PT New polypeptides (e.g. kinases, phosphatases, protease, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.

XX
PS Example 2; SEQ ID NO 1384; 134pp; English.

XX
CC The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at

```
CC fcp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 556 AA;
Query Match 100.0%; Score 79; DB 6; Length 556;
Best Local Similarity 100.0%; Pred. No. 3e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 ANSFVGTAGYVSPELL 16
Db 239 ANSFVGTAGYVSPELL 254

RESULT 28
ABU04712
ID ABU04712 standard; protein; 556 AA.
XX
AC ABU04712;
XX
DT 29-JAN-2003 (first entry)
XX
DE Human expressed protein tag (EPT) #1378.
XX
KM Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KM protease; protease inhibitor; transporter; cytoskeletal protein;
KM receptor; transcription factor; cancer; MHC;
KM major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KM adenocarcinoma; sarcoma; melanoma; lymphoma; leukemia.
XX
OS Homo sapiens.
XX
PN WO200278524-A2.
XX
PD 10-OCT-2002.
XX
PF 28-MAR-2002; 2002WO-US009671.
XX
PR 28-MAR-2001; 2001US-0279495P.
PR 21-MAY-2001; 2001US-0292544P.
PR 08-AUG-2001; 2001US-0310801P.
PR 01-OCT-2001; 2001US-0326370P.
PR 04-DEC-2001; 2001US-0336780P.
PR 20-FEB-2002; 2002US-0358985P.
XX
PA (ZYCO-) ZYCOS INC.
XX
PI Chicx RM, Tomlinson AJ, Urban RG;
XX
DR WPI; 2003-040607/03.
XX
PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX
PS Example 2; SEQ ID NO 1378; 134pp; English.
XX
CC The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
```

```
CC fcp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 556 AA;
Query Match 100.0%; Score 79; DB 6; Length 556;
Best Local Similarity 100.0%; Pred. No. 3e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 ANSFVGTAGYVSPELL 16
Db 239 ANSFVGTAGYVSPELL 254

RESULT 29
ABU04716
ID ABU04716 standard; protein; 556 AA.
XX
AC ABU04716;
XX
DT 29-JAN-2003 (first entry)
XX
DE Human expressed protein tag (EPT) #1382.
XX
KM Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KM protease; protease inhibitor; transporter; cytoskeletal protein;
KM receptor; transcription factor; cancer; MHC;
KM major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KM adenocarcinoma; sarcoma; melanoma; lymphoma; leukemia.
XX
OS Homo sapiens.
XX
PN WO200278524-A2.
XX
PD 10-OCT-2002.
XX
PF 28-MAR-2002; 2002WO-US009671.
XX
PR 28-MAR-2001; 2001US-0279495P.
PR 21-MAY-2001; 2001US-0292544P.
PR 08-AUG-2001; 2001US-0310801P.
PR 01-OCT-2001; 2001US-0326370P.
PR 04-DEC-2001; 2001US-0336780P.
PR 20-FEB-2002; 2002US-0358985P.
XX
PA (ZYCO-) ZYCOS INC.
XX
PI Chicx RM, Tomlinson AJ, Urban RG;
XX
DR WPI; 2003-040607/03.
XX
PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX
PS Example 2; SEQ ID NO 1382; 134pp; English.
XX
CC The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
```

```
CC fcp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 556 AA;
Query Match 100.0%; Score 79; DB 6; Length 556;
Best Local Similarity 100.0%; Pred. No. 3e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ANSFVGTGAQYVSPPELL 16
Db 239 ANSFVGTGAQYVSPPELL 254

RESULT 30
ABU04711
ID ABU04711 standard; protein; 556 AA.
XX
AC ABU04711;
XX
DT 29-JAN-2003 (first entry)
XX
DE Human expressed protein tag (EPT) #1377.
XX
KM Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KM protease; protease inhibitor; transporter; cytoskeletal protein;
KM receptor; transcription factor; cancer; MHC;
KM major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KM adenocarcinoma; sarcoma; melanoma; lymphoma; leukemia.
XX
OS Homo sapiens.
XX
PN WO200278524-A2.
XX
PD 10-OCT-2002.
XX
PF 28-MAR-2002; 2002MO-US009671.
XX
PR 28-MAR-2001; 2001US-0279495P.
PR 21-MAY-2001; 2001US-0292544P.
PR 08-AUG-2001; 2001US-0310801P.
PR 01-OCT-2001; 2001US-0326370P.
PR 04-DEC-2001; 2001US-0336780P.
PR 20-FEB-2002; 2002US-0358985P.
XX
PA (ZYCO-) ZYCOS INC.
XX
PI Chiciz RM, Tomlinson AJ, Urban RG;
XX
DR WPI; 2003-040607/03.
XX
PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX
PS Example 2; SEQ ID NO 1377; 134pp; English.
XX
CC The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
```

```
CC fcp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 556 AA;
Query Match 100.0%; Score 79; DB 6; Length 556;
Best Local Similarity 100.0%; Pred. No. 3e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ANSFVGTGAQYVSPPELL 16
Db 239 ANSFVGTGAQYVSPPELL 254

RESULT 31
ABU04706
ID ABU04706 standard; protein; 556 AA.
XX
AC ABU04706;
XX
DT 29-JAN-2003 (first entry)
XX
DE Human expressed protein tag (EPT) #1372.
XX
KM Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KM protease; protease inhibitor; transporter; cytoskeletal protein;
KM receptor; transcription factor; cancer; MHC;
KM major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KM adenocarcinoma; sarcoma; melanoma; lymphoma; leukemia.
XX
OS Homo sapiens.
XX
PN WO200278524-A2.
XX
PD 10-OCT-2002.
XX
PF 28-MAR-2002; 2002MO-US009671.
XX
PR 28-MAR-2001; 2001US-0279495P.
PR 21-MAY-2001; 2001US-0292544P.
PR 08-AUG-2001; 2001US-0310801P.
PR 01-OCT-2001; 2001US-0326370P.
PR 04-DEC-2001; 2001US-0336780P.
PR 20-FEB-2002; 2002US-0358985P.
XX
PA (ZYCO-) ZYCOS INC.
XX
PI Chiciz RM, Tomlinson AJ, Urban RG;
XX
DR WPI; 2003-040607/03.
XX
PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX
PS Example 2; SEQ ID NO 1372; 134pp; English.
XX
CC The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
```



```
CC ffp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 556 AA;
Query Match 100.0%; Score 79; DB 6; Length 556;
Best Local Similarity 100.0%; Pred. No. 3e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ANSFVGTAGQYVSPELL 16
   |||||
Db 239 ANSFVGTAGQYVSPELL 254

RESULT 32
ABU04714
ID ABU04714 standard; protein; 556 AA.
XX
AC ABU04714;
XX
DT 29-JAN-2003 (first entry)
XX
DE Human expressed protein tag (EPT) #1380.
XX
KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukemia.
XX
OS Homo sapiens.
XX
PN WO200278524-A2.
XX
PD 10-OCT-2002.
XX
PE 28-MAR-2002; 2002WO-US009671.
XX
PR 28-MAR-2001; 2001US-0279495P.
PR 21-MAY-2001; 2001US-0292544P.
PR 08-AUG-2001; 2001US-0310801P.
PR 01-OCT-2001; 2001US-0326370P.
PR 04-DEC-2001; 2001US-0336780P.
PR 20-FEB-2002; 2002US-0358985P.
XX
PA (ZYCO-) ZYCOS INC.
XX
PI Chicx RM, Tomlinson AJ, Urban RG;
XX
DR WPI; 2003-040607/03.
XX
PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX
PS Example 2; SEQ ID NO 1380; 134pp; English.
XX
CC The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
```

```
CC ffp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 556 AA;
Query Match 100.0%; Score 79; DB 6; Length 556;
Best Local Similarity 100.0%; Pred. No. 3e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ANSFVGTAGQYVSPELL 16
   |||||
Db 239 ANSFVGTAGQYVSPELL 254

RESULT 33
ABU04707
ID ABU04707 standard; protein; 556 AA.
XX
AC ABU04707;
XX
DT 29-JAN-2003 (first entry)
XX
DE Human expressed protein tag (EPT) #1373.
XX
KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukemia.
XX
OS Homo sapiens.
XX
PN WO200278524-A2.
XX
PD 10-OCT-2002.
XX
PE 28-MAR-2002; 2002WO-US009671.
XX
PR 28-MAR-2001; 2001US-0279495P.
PR 21-MAY-2001; 2001US-0292544P.
PR 08-AUG-2001; 2001US-0310801P.
PR 01-OCT-2001; 2001US-0326370P.
PR 04-DEC-2001; 2001US-0336780P.
PR 20-FEB-2002; 2002US-0358985P.
XX
PA (ZYCO-) ZYCOS INC.
XX
PI Chicx RM, Tomlinson AJ, Urban RG;
XX
DR WPI; 2003-040607/03.
XX
PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX
PS Example 2; SEQ ID NO 1373; 134pp; English.
XX
CC The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
```

CC fcp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 556 AA;
Query Match 100.0%; Score 79; DB 6; Length 556;
Best Local Similarity 100.0%; Pred. No. 3e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ANSFVGTAAQYVSPDLL 16
| | | | | | | | | | | | | | | | | | | | | |
DB 239 ANSFVGTAAQYVSPDLL 254
RESULT 34
ABU04717
ID ABU04717 standard; protein; 556 AA.
XX
AC ABU04717;
XX
DT 29-JAN-2003 (first entry)
XX
DE Human expressed protein tag (EPT) #1383.
XX
KM Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KM protease; protease inhibitor; transporter; cytoskeletal protein;
KM receptor; transcription factor; cancer; MHC;
KM major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KM adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX
OS Homo sapiens.
XX
PN WO200278524-A2.
XX
PD 10-OCT-2002.
XX
PF 28-MAR-2002; 2002WO-US009671.
XX
PR 28-MAR-2001; 2001US-0279495P.
PR 21-MAY-2001; 2001US-0292544P.
PR 08-AUG-2001; 2001US-0310801P.
PR 01-OCT-2001; 2001US-0326370P.
PR 04-DEC-2001; 2001US-0336780P.
PR 20-FEB-2002; 2002US-0358985P.
XX
PA (ZYCO-) ZYCOs INC.
XX
PI Chicz RM, Tomlinson AJ, Urban RG;
XX
DR WPI; 2003-040607/03.
XX
PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX
PS Example 2; SEQ ID NO 1383; 134pp; English.
XX
CC The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at

CC fcp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 556 AA;
Query Match 100.0%; Score 79; DB 6; Length 556;
Best Local Similarity 100.0%; Pred. No. 3e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ANSFVGTAAQYVSPDLL 16
| | | | | | | | | | | | | | | | | | | | | |
DB 239 ANSFVGTAAQYVSPDLL 254
RESULT 35
ABM79012
ID ABM79012 standard; protein; 556 AA.
XX
AC ABM79012;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human phosphoinositide dependent protein kinase 1.
XX
DE Human phosphoinositide dependent protein kinase 1.
XX
KM Human; phosphoinositide dependent protein kinase 1; PDPK1; enzyme; p53;
KM cytosolic; gene therapy.
XX
OS Homo sapiens.
XX
PN WO2003073823-A2.
XX
PD 12-SEP-2003.
XX
PF 28-FEB-2003; 2003WO-US006138.
XX
PR 01-MAR-2002; 2002US-0361196P.
XX
PA (EXEL-) EXELIXIS INC.
XX
PI Belvin M, Francis-Liang H, Friedman L, Plozman GD, Heuer TS;
XX
DR WPI; 2003-731639/69.
XX
DR N-PSDB; ACF80613.
XX
PT Identifying a candidate p53 pathway-modulating agent as therapeutic
PT targets for disorders related to defective p53 function e.g. cancer by
PT contacting an assay system having PDPK1 polypeptide or nucleic acid, with
PT a test agent.
XX
PS Claim 13; Page 49-53; 52pp; English.
XX
CC The present sequence is that of human phosphoinositide dependent protein
CC kinase 1 (PDPK1) polypeptide GI 4505695. Genetic screens were designed to
CC identify modifiers of the p53 pathway in Drosophila, where a genetic
CC screen was performed in which p53 was overexpressed in the wing. The
CC CG1210 gene was isolated as a modifier of the p53 pathway, and human
CC orthologues, termed PDPK1, were subsequently identified. The invention
CC provides methods for using these p53 modifier genes and the polypeptides
CC they encode to identify PDPK1-modulating agents that are candidate
CC therapeutic agents and can be used in the treatment of disorders
CC associated with defective or impaired p53 function and/or PDPK1 function,
CC such as angiogenic, apoptotic or cell proliferative disorders, e.g.
CC cancer. Preferred PDPK1-modulating agents specifically bind to PDPK1
CC polypeptides and restore p53 function. Other preferred PDPK1-modulating
CC agents are nucleic acid modulators such as antisense oligonucleotides and
CC RNAi that repress PDPK1 gene expression or product activity. PDPK1
CC modulating agents are useful in diagnosis, therapy and pharmaceutical
CC development
XX
SQ Sequence 556 AA;
Query Match 100.0%; Score 79; DB 7; Length 556;
Best Local Similarity 100.0%; Pred. No. 3e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ANSFVGTAQYVSPBL 16
| | | | | | | | | | | | | | | |
Db 239 ANSFVGTAQYVSPBL 254

RESULT 36
ADD44915
ID ADD44915 standard; protein; 556 AA.
XX
AC ADD44915;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human Protein NP_002604, SEQ ID NO 10350.
XX
KW Human; pain; neuronal tissue; gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; CCI;
KW spared nerve injury; SNI; Chung.
XX
OS Homo sapiens.
XX
PN WO2003016475-A2.
XX
PD 27-FEB-2003.
XX
PF 14-AUG-2002; 2002WO-US025765.
XX
PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
PA (GHEO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX
PI Woolf C, D'urso D, Befort K, Costigan M;
XX
DR WPI; 2003-268312/26.
DR GENBANK; NP_002604.
XX
PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
PS Claim 1; Page; 1017pp; English.

CC The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

SQ Sequence 556 AA;
Query Match 100.0%; Score 79; DB 7; Length 556;
Best Local Similarity 100.0%; Pred. No. 3e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ANSFVGTAQYVSPBL 16
| | | | | | | | | | | | | | | |
Db 239 ANSFVGTAQYVSPBL 254

RESULT 37
ADD44915
ID ADD44915 standard; protein; 556 AA.
XX
AC ADD44915;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human Protein NP_002604, SEQ ID NO 10346.
XX
KW Human; pain; neuronal tissue; gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; CCI;
KW spared nerve injury; SNI; Chung.
XX
OS Homo sapiens.
XX
PN WO2003016475-A2.
XX
PD 27-FEB-2003.
XX
PF 14-AUG-2002; 2002WO-US025765.
XX
PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
PA (GHEO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX
PI Woolf C, D'urso D, Befort K, Costigan M;
XX
DR WPI; 2003-268312/26.
DR GENBANK; NP_002604.
XX
PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
PS Claim 1; Page; 1017pp; English.

CC The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (shown in Table 2 of

CC the specification) which is differentially expressed during pain. Note:
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic form directly from WIPO at
 CC ftp.wipo.int/pub/published_pat_sequences.

XX Sequence 556 AA;

Query Match 100.0%; Score 79; DB 7; Length 556;
 Best Local Similarity 100.0%; Pred. No. 3e-05;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ANSFVGTAGYVSPBL 16
 |||||
 Db 239 ANSFVGTAGYVSPBL 254

RESULT 38
 ADD89983 ID ADD89983 standard; protein; 556 AA.

XX ADD89983;

XX 29-JAN-2004 (first entry)

XX Human cancer-associated protein kinase PDPK1.

XX PDPK1, protein kinase; enzyme; cancer; cytostatic; immunosuppressive;
 KM antidiabetic; antirheumatic; antiarthritic; antiproliferative;
 KM antiangiogenic; antiarteriosclerotic; antiinflammatory; vulnary;
 KM gynaecological; neuroprotective; gene therapy; human.

XX Homo sapiens.

XX W02003083096-A2.

XX 09-OCT-2003.

XX 21-MAR-2003; 2003WO-CA000409.

XX 28-MAR-2002; 2002US-0368853P.

XX (KINE-) KINETEK PHARM INC.

XX Delaney AD;

XX WPI; 2003-833542/77.

XX N-PSDB; ADD89982.

XX New nucleic acids encoding cancer associated protein kinases, useful as
 PT targets for screening pharmaceutical agents that inhibit the growth of
 PT tumor cells, or for diagnosing and treating cancer, inflammation or
 PT autoimmune disease.

XX Claim 1; Page 90-91; 91pp; English.

XX The present sequence is the protein sequence of the human cancer-
 CC associated protein kinase, PDPK1, an early component of the PI-3 kinase
 CC pathway. PDPK1 is one of a set of protein kinases that are shown by the
 CC invention to be over-expressed in hyper-proliferative cells. These
 CC protein kinases provide targets for drug screening for agents effective
 CC in inhibiting the growth or metastasis of tumour cells, and for
 CC determining other molecular targets in kinase signal transduction
 CC pathways involved in transformation and growth of tumour cells. A claimed
 CC method for inhibiting the growth of a cancer cell involves down-
 CC regulating the activity of the protein kinase using an antisense sequence
 CC or inhibitor of kinase activity, especially where the cancer cell is a
 CC breast, liver, colon, muscle, prostate, kidney, lung, placental or
 CC uterine cancer cell. Detection of over-expression in cancers provides a
 CC useful diagnostic for predicting patient prognosis and probability of
 CC drug effectiveness. Agents that specifically bind the protein kinases can
 CC be used for treatment and visualisation of tumours in patients. The
 CC protein kinase polypeptides and nucleic acids may also be used for
 CC treating hyperproliferative diseases, such as autoimmune disease,

CC diabetes mellitus, multiple sclerosis, rheumatoid arthritis, psoriasis,
 CC atherosclerosis, inflammation, scarring, endometriosis and angiogenesis.

XX Sequence 556 AA;

Query Match 100.0%; Score 79; DB 7; Length 556;
 Best Local Similarity 100.0%; Pred. No. 3e-05;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ANSFVGTAGYVSPBL 16
 |||||
 Db 239 ANSFVGTAGYVSPBL 254

RESULT 39
 ADI36055 ID ADI36055 standard; protein; 556 AA.

XX ADI36055;

XX 15-APR-2004 (first entry)

XX Human phosphoinositide dependent protein kinase (PDPK1) related protein.

XX PDPK1, p53 pathway; phosphoinositide dependent protein kinase 1; cancer;
 KM impaired p53 function; therapy; human.

XX Homo sapiens.

XX US2003215849-A1.

XX 20-NOV-2003.

XX 28-FEB-2003; 2003US-00376554.

XX 01-MAR-2002; 2002US-0361196P.

XX (BELV/) BELVIN M.

XX (FRAN/) FRANCIS-LANG H.

XX (FRIE/) FRIEDMAN L.

XX (PLOW/) PLOWMAN G D.

XX (HEUE/) HEUER T S.

XX Belvin M, Francis-Lang H, Friedman L, Plowman GD, Heuer TS;

XX WPI; 2004-154398/15.

XX Identifying a p53 pathway modulating agent by providing assay system
 PT comprising phosphoinositide dependent protein kinase 1, contacting assay
 PT system to test agent, detecting test agent-biased activity of assay
 PT system.

XX Claim 13; SEQ ID NO 6; 24pp; English.

XX The invention relates to a method for identifying a p53 pathway
 CC modulating agent. The method comprising providing an assay system
 CC comprising phosphoinositide dependent protein kinase 1 (PDPK1)
 CC polypeptide or polynucleotide, contacting the assay system with a test
 CC agent and detecting a test agent-biased activity of assay system, where a
 CC difference between the test agent-biased activity and the reference
 CC activity identifies the test agent as the modulating agent. The invention
 CC is useful for diagnosing disease such as cancer and for modulating p53
 CC pathway of a cell. The invention is useful in a variety of diagnostic and
 CC therapeutic applications where disease or disease prognosis is related to
 CC defects in the p53 pathway. The invention is useful for modulating PDPK1
 CC function in a cell and treating disorders associated with impaired p53
 CC function by administering the modulating agent that modulates p53
 CC pathway. The present sequence is human phosphoinositide dependent protein
 CC kinase (PDPK1) related protein.

XX Sequence 556 AA;

Query Match 100.0%; Score 79; DB 8; Length 556;

Best Local Similarity 100.0%; Pred. No. 3e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ANSFVGTGAQYVSPBL 16
|||||
Db 239 ANSFVGTGAQYVSPBL 254

RESULT 40

AD015485
ID AD015485 standard; protein; 556 AA.

AC AD015485;

DT 12-AUG-2004 (first entry)

XX Human PDPK1 protein that interacts with PKC theta SeqID 14.

XX human; effector T-cell; regulatory T-cell; protein kinase C theta;

KM PKC theta; inflammatory cytokine; cellular proliferation; PRKC;

KM nck-theta; PRKC; gene therapy; allergic disorder; autoimmune disorder;

KM infection; cancer; vaccine; antiallergic; antibacterial; antiparasitic;

XX cytoskeletal; immunosuppressive; virucidal; PDPK1.

XX Homo sapiens.

XX MO2004043386-A2.

XX 27-MAY-2004.

XX 10-NOV-2003; 2003MO-US035719.

XX 08-NOV-2002; 2002US-0424777P.

XX 02-MAY-2003; 2003US-0467477P.

XX (TOL-E-) TOLERRX INC.

XX Rao P;

XX WPI; 2004-411627/38.

XX N-PSDB; AD015484.

XX Treating a condition such as an allergic or autoimmune disorder, a viral

PT infection or cancer; comprises administering an agent that modulates the

PT expression or activity of a protein kinase C theta (PKC theta) pathway

XX Example 3; SEQ ID NO 14; 88bp; English.

XX This invention relates to a novel agent that modulates the balance of

CC effector T-cell function relative to regulatory T-cell function in a

CC population of cells. Specifically, it refers to agents that can alter the

CC expression or activity of a protein kinase C theta (PKC theta) pathway

CC cytokines and cellular proliferation. Note that PKC theta is a serine

CC threonine protein kinase that is also known as PRKC, nck-theta and

CC PRKCQ. The present invention describes a gene therapy method useful for

CC treating conditions including an allergic disorder, an autoimmune

CC disorder, a viral, microbial or parasitic infection, as well as cancer or

CC treatment following a transplant because it provides a route to enhance

CC the immune response. Accordingly, compositions can be used to develop a

CC vaccine and furthermore they exhibit antiallergic, antibacterial,

CC antiparasitic, cytoskeletal, immunosuppressive and virucidal activities.

CC This polypeptide sequence is the human PDPK1 protein that interacts with

CC PKC-theta of the invention.

XX Sequence 556 AA;

XX Query Match 100.0%; Score 79; DB 8; Length 556;

XX Best Local Similarity 100.0%; Pred. No. 3e-05;

XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ANSFVGTGAQYVSPBL 16
|||||

Db 239 ANSFVGTGAQYVSPBL 254

RESULT 41

ADQ19234
ID ADQ19234 standard; protein; 556 AA.

AC ADQ19234;

DT 26-AUG-2004 (first entry)

XX Human soft tissue sarcoma-upregulated protein - SEQ ID 2053.

XX soft tissue sarcoma; cytoskeletal; gene therapy; vaccine; screening; human.

XX Homo sapiens.

XX MO2004048938-A2.

XX 10-JUN-2004.

XX 26-NOV-2003; 2003MO-US038193.

XX 26-NOV-2002; 2002US-0429739P.

XX (PROT-) PROTEIN DESIGN LABS INC.

XX Aziz N, Ginsburg WM, Zlotnik A;

XX WPI; 2004-441208/41.

XX Early detection of soft tissue sarcoma comprises determining expression

PT of a gene in a first soft tissue sample and a normal soft tissue sample

PT and comparing the gene expression, also useful in treating soft tissue

XX Example 2; SEQ ID NO 2053; 210bp; English.

XX The invention relates to a novel method for detecting soft tissue sarcoma

CC which comprises obtaining a first soft tissue sample from an individual

CC and a normal soft tissue sample from the same or different individual,

CC determining the expression of a gene in both samples and comparing the

CC expression of the gene in both soft tissue samples, where a higher level

CC of protein expression in the first soft tissue sample indicates the

CC presence of soft tissue sarcoma. The method of the invention has

CC cytoskeletal applications and may be useful for detecting soft tissue

CC sarcoma, possibly via gene therapy or vaccine production. The nucleic

CC acid sequences may be useful in diagnostic and screening applications.

CC The current sequence is that of a human soft tissue sarcoma-upregulated

CC protein of the invention. The current sequence is not shown within the

CC specification per se but was submitted in CD format by the inventor.

XX Sequence 556 AA;

XX Query Match 100.0%; Score 79; DB 8; Length 556;

XX Best Local Similarity 100.0%; Pred. No. 3e-05;

XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ANSFVGTGAQYVSPBL 16
|||||

XX ADD44917 standard; protein; 559 AA.

XX ADD44917;

XX 29-JAN-2004 (first entry)

XX Rat Protein O55173, SEQ ID NO 10348.

KM Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
 KM chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
 OS Rattus norvegicus.
 PN WO2003016475-A2.
 XX
 PD 27-FEB-2003.
 XX
 PF 14-AUG-2002; 2002WO-US025765.
 XX
 PR 14-AUG-2001; 2001US-0312147P.
 PR 01-NOV-2001; 2001US-0346382P.
 PR 26-NOV-2001; 2001US-0333347P.
 XX
 PA (GEHO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 XX
 PI Woolf C, D'urso D, Befort K, Costigan M;
 DR WPI; 2003-268312/26.
 DR GENBANK; 055173.
 XX
 PT New composition comprising two or more isolated polypeptides, useful for
 PT preparing a medicament for treating pain in an animal.
 XX
 PS Claim 1; Page; 1017p; English.
 XX
 CC The invention discloses a composition comprising two or more isolated rat
 CC or human polynucleotides or a polynucleotide which represents a fragment,
 CC derivative or allelic variation of the nucleic acid sequence. Also
 CC claimed are a vector comprising the novel polynucleotide, a host cell
 CC comprising the vector, a method for identifying a nucleotide sequence
 CC which is differentially regulated in an animal subjected to pain and a
 CC kit to perform the method, an array, a method for identifying an agent
 CC that increases or decreases the expression of the polynucleotide sequence
 CC that is differentially expressed in neuronal tissue of a first animal
 CC subjected to pain, a method for identifying a compound which regulates
 CC the expression of a polynucleotide sequence which is differentially
 CC expressed in an animal subjected to pain, a method for identifying a
 CC compound that regulates the activity of one or more of the
 CC polynucleotides, a method for producing a pharmaceutical composition, a
 CC method for identifying a compound or small molecule that regulates the
 CC activity in an animal of one or more of the polypeptides given in the
 CC specification, a method for identifying a compound useful in treating
 CC pain and a pharmaceutical composition comprising the one or more
 CC polypeptides or their antibodies. The polynucleotide or the compound that
 CC modulates its activity is useful for preparing a medicament for treating
 CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
 CC therapy). The sequence presented is a rat protein (shown in Table 2 of
 CC the specification) which is differentially expressed during pain. Note:
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic form directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 CC
 XX Sequence 559 AA;
 SQ
 QY Query Match 100.0%; Score 79; DB 7; Length 559;
 Db Best Local Similarity 100.0%; Pred. No. 3e-05;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 ANSFVGTRQYVSPBL 16
 ||||||||||||
 242 ANSFVGTRQYVSPBL 257
 RESULT 43
 ADD44913 standard; protein; 559 AA.
 ID ADD44913
 XX AC ADD44913;
 XX

DT 29-JAN-2004 (first entry)
 XX
 DE Rat Protein 055173, SEQ ID NO 10344.
 XX
 KM Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
 KM chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
 OS Rattus norvegicus.
 PN WO2003016475-A2.
 XX
 PD 27-FEB-2003.
 XX
 PF 14-AUG-2002; 2002WO-US025765.
 XX
 PR 14-AUG-2001; 2001US-0312147P.
 PR 01-NOV-2001; 2001US-0346382P.
 PR 26-NOV-2001; 2001US-0333347P.
 XX
 PA (GEHO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 XX
 PI Woolf C, D'urso D, Befort K, Costigan M;
 DR WPI; 2003-268312/26.
 DR GENBANK; 055173.
 XX
 PT New composition comprising two or more isolated polypeptides, useful for
 PT preparing a medicament for treating pain in an animal.
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 PS Claim 1; Page; 1017p; English.
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 CC or human polynucleotides or a polynucleotide which represents a fragment,
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 CC comprising the vector, a method for identifying a nucleotide sequence
 CC which is differentially regulated in an animal subjected to pain and a
 CC kit to perform the method, an array, a method for identifying an agent
 CC that increases or decreases the expression of the polynucleotide sequence
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 CC subjected to pain, a method for identifying a compound which regulates
 CC the expression of a polynucleotide sequence which is differentially
 CC expressed in an animal subjected to pain, a method for identifying a
 CC compound that regulates the activity of one or more of the
 CC polynucleotides, a method for producing a pharmaceutical composition, a
 CC method for identifying a compound or small molecule that regulates the
 CC activity in an animal of one or more of the polypeptides given in the
 CC specification, a method for identifying a compound useful in treating
 CC pain and a pharmaceutical composition comprising the one or more
 CC polypeptides or their antibodies. The polynucleotide or the compound that
 CC modulates its activity is useful for preparing a medicament for treating
 CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
 CC therapy). The sequence presented is a rat protein (shown in Table 2 of
 CC the specification) which is differentially expressed during pain. Note:
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic form directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 CC
 XX Sequence 559 AA;
 SQ
 QY Query Match 100.0%; Score 79; DB 7; Length 559;
 Db Best Local Similarity 100.0%; Pred. No. 3e-05;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 ANSFVGTRQYVSPBL 16
 ||||||||||||
 242 ANSFVGTRQYVSPBL 257

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OM protein - protein search, using ew model

Run on: May 16, 2006, 13:28:04 ; Search time 46 Seconds

(without alignments)
28.757 Million cell updates/sec

Title: US-10-689-576-3

Sequence: 79
1 ANSFVGTAYVSPRL 16Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*

- 1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*
- 2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
- 3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
- 4: /cgn2_6/ptodata/1/iaa/PCRTUS_COMB.pep:*
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- 6: /cgn2_6/ptodata/1/iaa/backfilest1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	79	100.0	15	2	US-08-943-667-3
2	79	100.0	25	2	US-09-205-658-185
3	79	100.0	98	2	US-09-205-658-196
4	79	100.0	556	1	US-09-016-000-4
5	79	100.0	556	2	US-09-156-793D-2
6	79	100.0	556	2	US-08-943-667-1
7	79	100.0	556	2	US-09-771-161A-245
8	70	88.6	788	2	US-09-248-796A-20511
9	67	84.8	766	2	US-09-538-092-216
10	66	83.5	752	2	US-08-943-667-29
11	66	83.5	901	2	US-09-248-796A-20495
12	60	75.9	228	2	US-09-755-665-38
13	60	75.9	234	2	US-09-384-162-9
14	60	75.9	368	1	US-08-423-399B-35
15	60	75.9	389	2	US-09-755-665-36
16	60	75.9	392	2	US-09-538-092-1257
17	60	75.9	393	1	US-08-423-399B-33
18	60	75.9	393	1	US-08-530-950-11
19	60	75.9	393	2	US-08-888-429A-11
20	60	75.9	393	2	US-09-149-878-11
21	60	75.9	393	2	US-09-057-009-11
22	60	75.9	393	2	US-09-593-653-11
23	60	75.9	400	1	US-08-878-989-17
24	60	75.9	400	2	US-09-272-796-17
25	60	75.9	404	2	US-09-949-016-7963
26	58	73.4	26	2	US-09-871-889A-7
27	58	73.4	27	2	US-09-311-311C-8

28	58	73.4	259	2	US-09-248-796A-18507	Sequence 18507, A
29	58	73.4	756	1	US-08-887-518-4	Sequence 4, Appli
30	58	73.4	756	1	US-09-023-321-4	Sequence 2, Appli
31	58	73.4	756	1	US-08-890-853-2	Sequence 2, Appli
32	58	73.4	756	1	US-09-032-475-4	Sequence 4, Appli
33	58	73.4	756	1	US-09-099-125A-2	Sequence 2, Appli
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36	58	73.4	756	2	US-08-890-854-2	Sequence 2, Appli
37	58	73.4	756	2	US-09-023-324-2	Sequence 2, Appli
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39	58	73.4	756	2	US-08-910-820-9	Sequence 9, Appli
40	58	73.4	756	2	US-09-109-986-2	Sequence 2, Appli
41	58	73.4	756	2	US-09-844-908-9	Sequence 9, Appli
42	58	73.4	756	2	US-08-868-758-4	Sequence 4, Appli
43	58	73.4	756	2	US-09-796-872-15	Sequence 15, Appli
44	58	73.4	756	2	US-09-771-161A-232	Sequence 232, App
45	57	72.2	25	2	US-09-205-658-187	Sequence 187, App

ALIGNMENTS

RESULT 1
US-08-943-667-3
Sequence 3, Application US/08943667
Patent No. 6734001
GENERAL INFORMATION:
APPLICANT: Alessi, Dario R
TITLE OF INVENTION: ENZYME
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESSES:
ADDRESSEE: ueckle Fleischmann & Muegel, LLP
STREET: 39 State Street
CITY: Rochester
STATE: New York
COUNTRY: USA
ZIP: 14614-1310
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943,667
FILING DATE: 03-OCT-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9705462.1
FILING DATE: 17-MAR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9712826.8
FILING DATE: 19-JUN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9717253.0
FILING DATE: 15-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: Braham, Susan J
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 87792.97R421
TELEPHONE: 716-262-3640
TELEFAX: 716-262-4133
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal

US-08-943-667-3

Query Match

Best Local Similarity 100.0%; Score 79; DB 2; Length 16;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ANSFVGTAGYVSPBL 16

Db 1 ANSFVGTAGYVSPBL 16

RESULT 2

US-09-205-658-185

; Sequence 185, Application US/09205658

; Patent No. 6861256

; GENERAL INFORMATION:

; APPLICANT: Ruvkun, Gary

; APPLICANT: Osg, Scott

; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR

; FILE REFERENCE: 00786/351004

; CURRENT APPLICATION NUMBER: US/09/205,658

; EARLIER FILING DATE: 1998-12-03

; EARLIER APPLICATION NUMBER: 08/857,076

; EARLIER FILING DATE: 1997-05-15

; EARLIER APPLICATION NUMBER: 08/888,534

; EARLIER FILING DATE: 1997-07-07

; EARLIER APPLICATION NUMBER: US98/10080

; NUMBER OF SEQ ID NOS: 328

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 185

; LENGTH: 25

; TYPE: PRT

; ORGANISM: Mus musculus or Homo sapiens

US-09-205-658-185

Query Match

Best Local Similarity 100.0%; Score 79; DB 2; Length 25;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ANSFVGTAGYVSPBL 16

Db 8 ANSFVGTAGYVSPBL 23

RESULT 3

US-09-205-658-196

; Sequence 196, Application US/09205658

; Patent No. 6861256

; GENERAL INFORMATION:

; APPLICANT: Ruvkun, Gary

; APPLICANT: Osg, Scott

; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR

; FILE REFERENCE: 00786/351004

; CURRENT APPLICATION NUMBER: US/09/205,658

; EARLIER FILING DATE: 1998-12-03

; EARLIER APPLICATION NUMBER: 08/857,076

; EARLIER FILING DATE: 1997-05-15

; EARLIER APPLICATION NUMBER: 08/888,534

; EARLIER FILING DATE: 1997-07-07

; EARLIER APPLICATION NUMBER: US98/10080

; NUMBER OF SEQ ID NOS: 328

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 196

; LENGTH: 98

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-205-658-196

Best Local Similarity 100.0%; Pred. No. 5.4e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ANSFVGTAGYVSPBL 16

Db 7 ANSFVGTAGYVSPBL 22

RESULT 4

US-09-016-000-4

; Sequence 4, Application US/09016000

; Patent No. 5962232

; GENERAL INFORMATION:

; APPLICANT: Hillman, Jennifer L.

; APPLICANT: Lal, Preeti

; APPLICANT: Bandman, Olga

; APPLICANT: Akerblom, Ingrid E.

; APPLICANT: Shah, Purvi

; APPLICANT: Corley, Neil C.

; TITLE OF INVENTION: PROTEIN KINASE MOLECULES

; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESSES:

; ADDRESSEE: Incyte Pharmaceuticals, Inc.

; STREET: 3174 Porter Drive

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq for Windows Version 2.0

; CURRENT APPLICATION DATA:

; FILING DATE: HEREWITH

; APPLICATION NUMBER: US/09/016,000

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Billings, Lucy J

; REGISTRATION NUMBER: 36,749

; REFERENCE/DOCKET NUMBER: PF-0465 US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 650-855-0555

; TELEFAX: 650-845-4166

; TELEX:

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 556 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; IMMEDIATE SOURCE:

; LIBRARY: MMLRIDT01

; CLONE: 472480

US-09-016-000-4

Query Match

Best Local Similarity 100.0%; Score 79; DB 1; Length 556;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ANSFVGTAGYVSPBL 16

Db 239 ANSFVGTAGYVSPBL 254

RESULT 5

US-09-156-793D-2

; Sequence 2, Application US/09156793D

; Patent No. 6682920

Query Match

100.0%; Score 79; DB 2; Length 98;

```

; GENERAL INFORMATION:
; APPLICANT: Stephens, Len
; APPLICANT: Hawkins, Philip T.
; APPLICANT: Stokoe, David
; TITLE OF INVENTION: Compositions and Methods for Identifying PKB Kinase
; TITLE OF INVENTION: Inhibitors
; FILE REFERENCE: 1030-US
; CURRENT APPLICATION NUMBER: US/09/156,793D
; CURRENT FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: 60/060,190
; PRIOR FILING DATE: 1997-09-26
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 556
; TYPE: PRT
; ORGANISM: PKB Kinase
; US-09-156-793D-2

Query Match      100.0%; Score 79; DB 2; Length 556;
Best Local Similarity 100.0%; Pred. No. 3.8e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ANSFVGTAGYVSPRL 16
Db      239 ANSFVGTAGYVSPRL 254

RESULT 6
US-08-943-667-1
; Sequence 1, Application US/08943667
; Patent No. 6734001
; GENERAL INFORMATION:
; APPLICANT: Aleesi, Darlo R
; TITLE OF INVENTION: ENZYME
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jaecle Fleischmann & Muegel, LLP
; STREET: 39 State Street
; CITY: Rochester
; STATE: New York
; COUNTRY: USA
; ZIP: 14614-1310
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/943,667
; FILING DATE: 03-OCT-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9705462.1
; FILING DATE: 17-MAR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9712826.8
; FILING DATE: 19-JUN-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9717253.0
; FILING DATE: 15-AUG-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Braham, Susan J
; REGISTRATION NUMBER: 34,103
; REFERENCE/DOCKET NUMBER: 87792.97R421
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 716-262-3640
; TELEFAX: 716-262-4133
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 556 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
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; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; US-08-943-667-1

Query Match      100.0%; Score 79; DB 2; Length 556;
Best Local Similarity 100.0%; Pred. No. 3.8e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ANSFVGTAGYVSPRL 16
Db      239 ANSFVGTAGYVSPRL 254

RESULT 7
US-09-771-161A-245
; Sequence 245, Application US/09771161A
; Patent No. 6936450
; GENERAL INFORMATION:
; APPLICANT: LEVINE, et al.
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
; FILE REFERENCE: 802620-2005.1
; CURRENT APPLICATION NUMBER: US/09/771,161A
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/724,676
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 136776
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 135619
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 245
; LENGTH: 556
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-771-161A-245

Query Match      100.0%; Score 79; DB 2; Length 556;
Best Local Similarity 100.0%; Pred. No. 3.8e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ANSFVGTAGYVSPRL 16
Db      239 ANSFVGTAGYVSPRL 254

RESULT 8
US-09-248-796A-20511
; Sequence 20511, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Kelch Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 20511
; LENGTH: 788
; TYPE: PRT
; ORGANISM: Candida albicans
; US-09-248-796A-20511

Query Match      88.6%; Score 70; DB 2; Length 788;
```

Best Local Similarity 87.5%; Pred. No. 0.00026;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ANSFVGTAAQVSPPELL 16
DB 40 AKSFVGTAEYVSPPELL 55

RESULT 9

US-09-538-092-216
Sequence 216, Application US/09538092
Patent No. 6753314
GENERAL INFORMATION:
APPLICANT: Glot, Loic
APPLICANT: Mansfield, Traci A.
TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
FILE REFERENCE: 15966-542
CURRENT FILING DATE: US/09/538,092
CURRENT FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: 60/127,352
PRIOR FILING DATE: 1999-04-01
PRIOR APPLICATION NUMBER: 60/178,965
PRIOR FILING DATE: 2000-02-01
NUMBER OF SEQ ID NOS: 1387
SOFTWARE: CurapatsSeqFormat Version 0.9
SEQ ID NO 216
LENGTH: 766
TYPE: PRT
ORGANISM: Saccharomyces cerevisiae
FEATURE:
NAME/KEY: misc_feature
LOCATION: (0)..(0)
OTHER INFORMATION: Polypeptide Accession Number YDR490C
US-09-538-092-216

Query Match 84.8%; Score 67; DB 2; Length 766;
Best Local Similarity 81.2%; Pred. No. 0.00088;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ANSFVGTAAQVSPPELL 16
DB 294 SKSFVGTAEYVSPPELL 309

RESULT 10

US-08-943-667-29
Sequence 29, Application US/08943667
Patent No. 6734001
GENERAL INFORMATION:
APPLICANT: Aleasi, Dario R
TITLE OF INVENTION: ENZYME
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jaekle Fleischmann & Muegel, LLP
STREET: 39 State Street
CITY: Rochester
STATE: New York
COUNTRY: USA
ZIP: 14614-1310
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943,667
FILING DATE: 03-OCT-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9705462.1
FILING DATE: 17-MAR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9712826.8

FILING DATE: 19-JUN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9717253.0
FILING DATE: 15-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: Braman, Susan J
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 87792.97R421
TELECOMMUNICATION INFORMATION:
TELEPHONE: 716-262-3640
TELEFAX: 716-262-4133

INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 752 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Drosophila
US-08-943-667-29

Query Match 83.5%; Score 66; DB 2; Length 752;
Best Local Similarity 92.9%; Pred. No. 0.0013;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 SFVGTAAQVSPPELL 16
DB 385 SFVGTAAQVSPPELL 398

RESULT 11

US-09-248-796A-20495
Sequence 20495, Application US/09248796A
Patent No. 6747137
GENERAL INFORMATION:
APPLICANT: Keith Weinstein et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 20495
LENGTH: 901
TYPE: PRT
ORGANISM: Candida albicans
US-09-248-796A-20495

Query Match 83.5%; Score 66; DB 2; Length 901;
Best Local Similarity 92.9%; Pred. No. 0.0016;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 SFVGTAAQVSPPELL 16
DB 265 SFVGTAAQVSPPELL 278

RESULT 12

US-09-755-665-38
Sequence 38, Application US/09755665
Patent No. 6600019
GENERAL INFORMATION:
APPLICANT: Prayaga, Sudhirdas K.
APPLICANT: Majumder, Kumud
APPLICANT: Tallon, Bruce E.
APPLICANT: Spaderma, Steven K.

```

: APPLICANT: Spytek, Kimberly A.
: APPLICANT: MacDougall, John
: TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
: FILE REFERENCE: 15966-631
: CURRENT APPLICATION NUMBER: US/09/755,665
: CURRENT FILING DATE: 2001-08-14
: PRIOR APPLICATION NUMBER: U.S.S.N. 60/174,724
: PRIOR FILING DATE: 2000-01-06
: NUMBER OF SEQ ID NOS: 118
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 38
: LENGTH: 228
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-755-665-38

Query Match          75.9%; Score 60; DB 2; Length 228;
Best Local Similarity 75.0%; Pred. No. 0.0043;
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      1 ANSFVGTAAQVSPRL 16
      ||||| |:-||| |
Db      58 ANSFVGTSTVSPRL 73

RESULT 13
US-09-384-162-9
: Sequence 9, Application US/09384162
: Patent No. 6376747
: GENERAL INFORMATION:
: APPLICANT: Xing, Ti
: APPLICANT: Malik, Kamal
: APPLICANT: Martin-Heller, Teresa
: APPLICANT: Miki L., Brian
: TITLE OF INVENTION: No. 6376747e1 Plant-Derived Map Kinase Kinase
: FILE REFERENCE: 08-884280US
: CURRENT APPLICATION NUMBER: US/09/384,162
: CURRENT FILING DATE: 1999-08-27
: NUMBER OF SEQ ID NOS: 24
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 9
: LENGTH: 234
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-384-162-9

Query Match          75.9%; Score 60; DB 2; Length 234;
Best Local Similarity 75.0%; Pred. No. 0.0045;
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      1 ANSFVGTAAQVSPRL 16
      ||||| |:-||| |
Db      129 ANSFVGTSTVSPRL 144

RESULT 14
US-08-423-399B-35
: Sequence 35, Application US/08423399B
: Patent No. 5663314
: GENERAL INFORMATION:
: APPLICANT: Seger, R., Seger, D., Ahn, N.G., and Krebs, E.G.
: TITLE OF INVENTION: HUMAN SIGNAL TRANSDUCTION MARK KINASE
: NUMBER OF SEQUENCES: 36
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Christensen, O'Connor, Johnson and Kindness
: STREET: 1420 Fifth Avenue, Suite 2800
: CITY: Seattle
: STATE: Washington
: COUNTRY: USA
: ZIP: 98101-2347
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette-5.25 inch, 1.2mb storage
: COMPUTER: IBM PC/386 Compatible
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: OPERATING SYSTEM: MS-DOS 4.01
: SOFTWARE: Word for Windows-t
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/423,399B
: FILING DATE: April 18, 1995
: CLASSIFICATION: 536
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/980,608
: FILING DATE: No. 5663314ember 20, 1992
: ATTORNEY/AGENT INFORMATION:
: NAME: Sheiness, Diana K.
: REGISTRATION NUMBER: 35,356
: REFERENCE/DOCKET NUMBER: WRFO-1-8427
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 1-206-682-8100; 1-206-224-0712 (direct)
: TELEFAX: 1-206-224-0779
: TELEX: 4938023
: INFORMATION FOR SEQ ID NO: 35:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 368 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: polypeptide
: DESCRIPTION: MAPK1b protein; FIGURE 14B
US-08-423-399B-35

Query Match          75.9%; Score 60; DB 1; Length 368;
Best Local Similarity 75.0%; Pred. No. 0.0074;
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      1 ANSFVGTAAQVSPRL 16
      ||||| |:-||| |
Db      194 ANSFVGTSTVSPRL 209

RESULT 15
US-09-755-665-36
: Sequence 36, Application US/09755665
: Patent No. 6600019
: GENERAL INFORMATION:
: APPLICANT: Prayaga, Sudhirdas K.
: APPLICANT: Majumder, Kunud
: APPLICANT: Tallon, Bruce E.
: APPLICANT: Spaderna, Steven K.
: APPLICANT: Spytek, Kimberly A.
: TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
: FILE REFERENCE: 15966-631
: CURRENT APPLICATION NUMBER: US/09/755,665
: CURRENT FILING DATE: 2001-08-14
: PRIOR APPLICATION NUMBER: U.S.S.N. 60/174,724
: PRIOR FILING DATE: 2000-01-06
: NUMBER OF SEQ ID NOS: 118
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 36
: LENGTH: 389
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-755-665-36

Query Match          75.9%; Score 60; DB 2; Length 389;
Best Local Similarity 75.0%; Pred. No. 0.0079;
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      1 ANSFVGTAAQVSPRL 16
      ||||| |:-||| |
Db      220 ANSFVGTSTVSPRL 235

Search completed: May 16, 2006, 13:29:23
Job time : 46 secs
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OM protein - protein search, using sw model

Run on: May 17, 2006, 13:06:00 ; Search time 0.001 Seconds
(without alignments)
328.040 Million cell updates/sec

Title: US-10-689-576-1
Perfect score: 2941
Sequence: 1 MARTTSQLYDAVPVIGSSVVL.....RKIGVWRQRYQSHHPDAVQ 556

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 4 seqs, 590 residues

Total number of hits satisfying chosen parameters: 4

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 4 summaries

Database : US10689576.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2941	100.0	556	1	US-10-689-576-1 Sequence 1, Appl 1
2	79	2.7	16	1	US-10-689-576-3 Sequence 3, Appl 1
3	52	1.8	10	1	US-10-689-576-4 Sequence 4, Appl 1
4	46	1.6	8	1	US-10-689-576-5 Sequence 5, Appl 1

ALIGNMENTS

RESULT 1
US-10-689-576-1
Sequence 1, Application US/10689576
GENERAL INFORMATION:
APPLICANT: Alesei, Dario R
TITLE OF INVENTION: ENZYME
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jaekle Fieleschmann & Muegel, LLP
STREET: 39 State Street
CITY: Rochester
STATE: New York
COUNTRY: USA
ZIP: 14614-1310
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/689,576
FILING DATE: 20-Oct-2003
CLASSIFICATION: 435
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/943,667
FILING DATE: 03-OCT-1997
APPLICATION NUMBER: GB 9705462.1
FILING DATE: 17-MAR-1997
APPLICATION NUMBER: GB 9712826.8
FILING DATE: 19-JUN-1997
APPLICATION NUMBER: GB 9717253.0
FILING DATE: 15-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: Braman, Susan J
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 87792,97R421
TELECOMMUNICATION INFORMATION:
TELEPHONE: 716-262-3640
TELEFAX: 716-262-4133
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 556 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-689-576-1

Query Match 100.0%; Score 2941; DB 1; Length 556;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MARTTSQLYDAVPVIGSSVVLCS	PSMVRTQTESSTPPGIPGSGRQGPAMDGTAAERRP	60
DB	1	MARTTSQLYDAVPVIGSSVVLCS	PSMVRTQTESSTPPGIPGSGRQGPAMDGTAAERRP	60
QY	61	GAGSLQHAOPPPQPKRRPDPFK	RGKILGSGSFSTVVLARELATRSRYAKILIEKRHIK	120
DB	61	GAGSLQHAOPPPQPKRRPDPFK	RGKILGSGSFSTVVLARELATRSRYAKILIEKRHIK	120
QY	121	ENKVPYTRRDVWSRLDHPFFV	KLYFTPODDEKLYFGLSYAKNGELIKYRKISFDET	180
DB	121	ENKVPYTRRDVWSRLDHPFFV	KLYFTPODDEKLYFGLSYAKNGELIKYRKISFDET	180
QY	181	CTREYTAIEVSALIEYLGKGI	IHRDLKPENILLNEDMHIQITDGTAKVLSPESKQARAN	240
DB	181	CTREYTAIEVSALIEYLGKGI	IHRDLKPENILLNEDMHIQITDGTAKVLSPESKQARAN	240
QY	241	SFVGTAGVSPBELITEKSACK	SDMLAGCIITQVLVAGLPFRAGNRYLIFOKIKLEYD	300
DB	241	SFVGTAGVSPBELITEKSACK	SDMLAGCIITQVLVAGLPFRAGNRYLIFOKIKLEYD	300
QY	301	PPEKFPKARDLVLEKLVLAT	ATKRLGCEMEGGLKAAHPFPESVTMENLHOOTPPKLT	360
DB	301	PPEKFPKARDLVLEKLVLAT	ATKRLGCEMEGGLKAAHPFPESVTMENLHOOTPPKLT	360
QY	361	YLPAMSEDDDCYGNYNLIS	OFQCMQVSSSSSHLSASDTGLPQSGSNIEQYIHLD	420
DB	361	YLPAMSEDDDCYGNYNLIS	OFQCMQVSSSSSHLSASDTGLPQSGSNIEQYIHLD	420
QY	421	SNSFELDLOFSEDEKRLLE	KQAGNPDWQFVENNLLKNGPVDKRGKLPARRQDLITE	480
DB	421	SNSFELDLOFSEDEKRLLE	KQAGNPDWQFVENNLLKNGPVDKRGKLPARRQDLITE	480
QY	481	GPHLYYDPPNKKYLGKGI	IPWSQELRPAAKNKPFVYTPRTYYLMDPSGNAHWCKRIQ	540
DB	481	GPHLYYDPPNKKYLGKGI	IPWSQELRPAAKNKPFVYTPRTYYLMDPSGNAHWCKRIQ	540
QY	541	EWWRQRYQSHHPDAVQ	556	
DB	541	EWWRQRYQSHHPDAVQ	556	

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RESULT 2
US-10-689-576-3
; Sequence 3, Application US/10689576
; GENERAL INFORMATION:
; APPLICANT: Aleesi, Dario R
; TITLE OF INVENTION: ENZYME
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jaackle Fleischmann & Mugel, LLP
; STREET: 39 State Street
; CITY: Rochester
; STATE: New York
; COUNTRY: USA
; ZIP: 14614-1310
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/689,576
; FILING DATE: 20-Oct-2003
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/943,667
; FILING DATE: 03-Oct-1997
; APPLICATION NUMBER: GB 9705462.1
; FILING DATE: 17-MAR-1997
; APPLICATION NUMBER: GB 9712826.8
; FILING DATE: 19-JUN-1997
; APPLICATION NUMBER: GB 9717253.0
; FILING DATE: 15-AUG-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Braham, Susan J
; REGISTRATION NUMBER: 34,103
; REFERENCE/DOCKET NUMBER: 87792,97R421
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 716-262-3640
; TELEFAX: 716-262-4133
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-689-576-3

Query Match      2.7%; Score 79; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      239 ANSFVGTAGYVSPELL 254
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Db      1 ANSFVGTAGYVSPELL 16

RESULT 3
US-10-689-576-4
; Sequence 4, Application US/10689576
; GENERAL INFORMATION:
; APPLICANT: Aleesi, Dario R
; TITLE OF INVENTION: ENZYME
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jaackle Fleischmann & Mugel, LLP
; STREET: 39 State Street
; CITY: Rochester
```

```
STATE: New York
COUNTRY: USA
ZIP: 14614-1310
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/689,576
; FILING DATE: 20-Oct-2003
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/943,667
; FILING DATE: 03-Oct-1997
; APPLICATION NUMBER: GB 9705462.1
; FILING DATE: 17-MAR-1997
; APPLICATION NUMBER: GB 9712826.8
; FILING DATE: 19-JUN-1997
; APPLICATION NUMBER: GB 9717253.0
; FILING DATE: 15-AUG-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Braham, Susan J
; REGISTRATION NUMBER: 34,103
; REFERENCE/DOCKET NUMBER: 87792,97R421
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 716-262-3640
; TELEFAX: 716-262-4133
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-689-576-4

Query Match      1.8%; Score 52; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      284 AGNEYLIFQK 293
      |||||||
Db      1 AGNEYLIFQK 10

RESULT 4
US-10-689-576-5
; Sequence 5, Application US/10689576
; GENERAL INFORMATION:
; APPLICANT: Aleesi, Dario R
; TITLE OF INVENTION: ENZYME
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jaackle Fleischmann & Mugel, LLP
; STREET: 39 State Street
; CITY: Rochester
; STATE: New York
; COUNTRY: USA
; ZIP: 14614-1310
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/689,576
; FILING DATE: 20-Oct-2003
; CLASSIFICATION: 435
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PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/943,667
FILING DATE: 03-OCT-1997
APPLICATION NUMBER: GB 9705462.1
FILING DATE: 17-MAR-1997
APPLICATION NUMBER: GB 9712826.8
FILING DATE: 19-JUN-1997
APPLICATION NUMBER: GB 9717253.0
FILING DATE: 15-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: Braman, Susan J
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 87792.97R421
TELECOMMUNICATION INFORMATION:
TELEPHONE: 716-262-3640
TELEFAX: 716-262-4133
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHEICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-689-576-5

Query Match 1.6%; Score 46; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 137 LDHPFPVK 144
|||||
Db 1 LDHPFPVK 8

Search completed: May 17, 2006, 13:06:00
Job time : 0.001 secs

GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 17, 2006, 13:06:00 ; Search time 0.001 Seconds
(without alignments)
9.440 Million cell updates/sec

Title: US-10-689-576-3

Perfect score: 79

Sequence: 1 ANSFVGTAGVSPRL 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 4 seqs, 590 residues

Total number of hits satisfying chosen parameters: 4

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 4 summaries

Database : US10689576.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	79	100.0	16 1 US-10-689-576-3	Sequence 3, Appli
2	79	100.0	566 1 US-10-689-576-1	Sequence 1, Appli
3	10	12.7	8 1 US-10-689-576-5	Sequence 5, Appli
4	10	12.7	10 1 US-10-689-576-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-10-689-576-3
Sequence 3, Application US/10689576
GENERAL INFORMATION:
APPLICANT: Aleesi, Dario R
TITLE OF INVENTION: ENZYME
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jaekle Fleischmann & Muegel, LLP
STREET: 39 State Street
CITY: Rochester
STATE: New York
COUNTRY: USA
ZIP: 14614-1310
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/689,576
FILING DATE: 20-Oct-2003
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/943,667
FILING DATE: 03-OCT-1997
APPLICATION NUMBER: GB 9705462.1
FILING DATE: 17-MAR-1997
APPLICATION NUMBER: GB 9712826.8
FILING DATE: 19-JUN-1997
APPLICATION NUMBER: GB 9717253.0
FILING DATE: 15-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: Braman, Susan J
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 87792.97R421
TELECOMMUNICATION INFORMATION:
TELEPHONE: 716-262-3640
TELEFAX: 716-262-4133
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHEICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-689-576-3
Query Match 100.0%; Score 79; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ANSFVGTAGVSPRL 16

Db 1 ANSFVGTAAQYVSPFL 16
|||||
RESULT 2
US-10-689-576-1
Sequence 1, Application US/10689576
GENERAL INFORMATION:
APPLICANT: Aleesi, Dario R
TITLE OF INVENTION: ENZYME
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Jaeckle Fleischmann & Muegel, LLP
STREET: 39 State Street
CITY: Rochester
STATE: New York
COUNTRY: USA
ZIP: 14614-1310
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/689,576
FILING DATE: 20-Oct-2003
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/943,667
FILING DATE: 03-Oct-1997
APPLICATION NUMBER: GB 9705462.1
FILING DATE: 17-MAR-1997
APPLICATION NUMBER: GB 9712826.8
FILING DATE: 19-JUN-1997
APPLICATION NUMBER: GB 9717253.0
FILING DATE: 15-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: Braman, Susan J
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 87792.97R421
TELECOMMUNICATION INFORMATION:
TELEPHONE: 716-262-3640
TELEFAX: 716-262-4133
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 556 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-689-576-1
Query Match 100.0%; Score 79; DB 1; Length 556;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ANSFVGTAAQYVSPFL 16
Db 239 ANSFVGTAAQYVSPFL 254
RESULT 3
US-10-689-576-5
Sequence 5, Application US/10689576
GENERAL INFORMATION:
APPLICANT: Aleesi, Dario R
TITLE OF INVENTION: ENZYME
NUMBER OF SEQUENCES: 35

CORRESPONDENCE ADDRESS:
ADDRESSEE: Jaeckle Fleischmann & Muegel, LLP
STREET: 39 State Street
CITY: Rochester
STATE: New York
COUNTRY: USA
ZIP: 14614-1310
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/689,576
FILING DATE: 20-Oct-2003
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/943,667
FILING DATE: 03-Oct-1997
APPLICATION NUMBER: GB 9705462.1
FILING DATE: 17-MAR-1997
APPLICATION NUMBER: GB 9712826.8
FILING DATE: 19-JUN-1997
APPLICATION NUMBER: GB 9717253.0
FILING DATE: 15-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: Braman, Susan J
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 87792.97R421
TELECOMMUNICATION INFORMATION:
TELEPHONE: 716-262-3640
TELEFAX: 716-262-4133
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHEICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-689-576-5
Query Match 12.7%; Score 10; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 FV 5
Db 6 FV 7
RESULT 4
US-10-689-576-4
Sequence 4, Application US/10689576
GENERAL INFORMATION:
APPLICANT: Aleesi, Dario R
TITLE OF INVENTION: ENZYME
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Jaeckle Fleischmann & Muegel, LLP
STREET: 39 State Street
CITY: Rochester
STATE: New York
COUNTRY: USA
ZIP: 14614-1310
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/689,576
 FILING DATE: 20-Oct-2003
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/943,667
 FILING DATE: 03-OCT-1997
 APPLICATION NUMBER: GB 9705462.1
 FILING DATE: 17-MAR-1997
 APPLICATION NUMBER: GB 9712826.8
 FILING DATE: 19-JUN-1997
 APPLICATION NUMBER: GB 9717253.0
 FILING DATE: 15-AUG-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Braman, Susan J
 REGISTRATION NUMBER: 34,103
 REFERENCE/DOCKET NUMBER: 87792.97R421
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 716-262-3640
 TELEFAX: 716-262-4133
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 10 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FRAGMENT TYPE: internal
 SEQUENCE DESCRIPTION: SEQ ID NO: 4:
 US-10-689-576-4

Query Match 12.7%; Score 10; DB 1; Length 10;
 Best Local Similarity 25.0%; Pred. No. 0;
 Matches 1; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 NSPV 5
 1 :
 DB 3 NEYL 6

Search completed: May 17, 2006, 13:06:00
 Job time : 0.001 secs

GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 17, 2006, 13:06:00 ; Search time 0.001 Seconds
 (without alignments)
 5.900 Million cell updates/sec

Title: US-10-689-576-4
 Perfect score: 52
 Sequence: 1 AGNEYLRFQK 10

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 4 seqs, 590 residues

Total number of hits satisfying chosen parameters: 4

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 4 summaries

Database : US10689576.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	52	100.0	10	1	US-10-689-576-4 Sequence 4, Appli
2	52	100.0	556	1	US-10-689-576-1 Sequence 1, Appli
3	10	19.2	8	1	US-10-689-576-5 Sequence 5, Appli
4	10	19.2	16	1	US-10-689-576-3 Sequence 3, Appli

ALIGNMENTS

RESULT 1
 US-10-689-576-4
 ; Sequence 4, Application US/10689576
 ; GENERAL INFORMATION:
 ; APPLICANT: Alesei, Dario R
 ; TITLE OF INVENTION: ENZYME
 ; NUMBER OF SEQUENCES: 35
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Jaekle Fieischmann & Muehl, LLP
 ; STREET: 39 State Street
 ; CITY: Rochester
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 14614-1310
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/10/689,576
 ; FILING DATE: 20-Oct-2003
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/943,667
 ; FILING DATE: 03-OCT-1997
 ; APPLICATION NUMBER: GB 9705462.1
 ; FILING DATE: 17-MAR-1997
 ; APPLICATION NUMBER: GB 9712826.8
 ; FILING DATE: 19-JUN-1997
 ; APPLICATION NUMBER: GB 9717253.0
 ; FILING DATE: 15-AUG-1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Braman, Susan J
 ; REGISTRATION NUMBER: 34,103
 ; REFERENCE/DOCKET NUMBER: 87792.97R421
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 716-262-3640
 ; TELEFAX: 716-262-4133
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 10 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; FRAGMENT TYPE: internal
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
 ; US-10-689-576-4

Query Match 100.0%; Score 52; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGNEYLIFOK 10
Db 1 AGNEYLIFOK 10

RESULT 2

US-10-689-576-1
; Sequence 1, Application US/10689576
; GENERAL INFORMATION:
; APPLICANT: Aleesi, Dario R
; TITLE OF INVENTION: ENZYME
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Jaekle Fleischmann & Muegel, LLP
; STREET: 39 State Street
; CITY: Rochester
; STATE: New York
; COUNTRY: USA
; ZIP: 14614-1310
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/689,576
; FILING DATE: 20-Oct-2003
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/943,667
; FILING DATE: 03-Oct-1997
; APPLICATION NUMBER: GB 9705462.1
; FILING DATE: 17-MAR-1997
; APPLICATION NUMBER: GB 9712826.8
; FILING DATE: 19-JUN-1997
; APPLICATION NUMBER: GB 9717253.0
; FILING DATE: 15-AUG-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Bramean, Susan J
; REGISTRATION NUMBER: 34,103
; REFERENCE/DOCKET NUMBER: 87792.97R421
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 716-262-3640
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 556 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-689-576-1

Query Match 100.0%; Score 52; DB 1; Length 556;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGNEYLIFOK 10
Db 284 AGNEYLIFOK 293

RESULT 3
US-10-689-576-5
; Sequence 5, Application US/10689576

GENERAL INFORMATION:

APPLICANT: Aleesi, Dario R
TITLE OF INVENTION: ENZYME
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Jaekle Fleischmann & Muegel, LLP
STREET: 39 State Street
CITY: Rochester
STATE: New York
COUNTRY: USA
ZIP: 14614-1310
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/689,576
FILING DATE: 20-Oct-2003
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/943,667
FILING DATE: 03-Oct-1997
APPLICATION NUMBER: GB 9705462.1
FILING DATE: 17-MAR-1997
APPLICATION NUMBER: GB 9712826.8
FILING DATE: 19-JUN-1997
APPLICATION NUMBER: GB 9717253.0
FILING DATE: 15-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: Bramean, Susan J
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 87792.97R421
TELECOMMUNICATION INFORMATION:
TELEPHONE: 716-262-3640
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-689-576-5

Query Match 19.2%; Score 10; DB 1; Length 8;
Best Local Similarity 28.6%; Pred. No. 0;
Matches 2; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 4 EYLIFOK 10
Db 2 DHPFFVK 8

RESULT 4
US-10-689-576-3
; Sequence 3, Application US/10689576
; GENERAL INFORMATION:
; APPLICANT: Aleesi, Dario R
; TITLE OF INVENTION: ENZYME
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Jaekle Fleischmann & Muegel, LLP
; STREET: 39 State Street
; CITY: Rochester
; STATE: New York
; COUNTRY: USA
; ZIP: 14614-1310
; COMPUTER READABLE FORM:

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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/689,576
FILING DATE: 20-Oct-2003
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/943,667
FILING DATE: 03-OCT-1997
APPLICATION NUMBER: GB 9705462.1
FILING DATE: 17-MAR-1997
APPLICATION NUMBER: GB 9712826.8
FILING DATE: 19-JUN-1997
APPLICATION NUMBER: GB 9717253.0
FILING DATE: 15-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: Braman, Susan J
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 87792.97R421
TELECOMMUNICATION INFORMATION:
TELEPHONE: 716-262-3640
TELEFAX: 716-262-4133
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-689-576-3

Query Match      19.2%  Score 10;  DB 1;  Length 16;
Best Local Similarity 25.0%  Pred. No. 0;
Matches 1; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Q# 3 NEYL 6
Db 2 NSFV 5

Search completed: May 17, 2006, 13:06:00
Job time : 0.001 secs

GenCore version 5.1.8
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OM protein - protein search, using sw model
Run on: May 17, 2006, 13:06:00 ; Search time 0.001 Seconds
(without alignments)
4.720 Million cell updates/sec

Title: US-10-689-576-5
Perfect score: 46
Sequence: 1 LDHPFFVK 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 4 seqs, 590 residues

Total number of hits satisfying chosen parameters: 4

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 4 summaries

Database : US10689576.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	46	100.0	8 1 US-10-689-576-5	Sequence 5, Appl1
2	46	100.0	556 1 US-10-689-576-1	Sequence 1, Appl1
3	10	21.7	10 1 US-10-689-576-4	Sequence 4, Appl1
4	10	21.7	16 1 US-10-689-576-3	Sequence 3, Appl1

ALIGNMENTS

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RESULT 1
US-10-689-576-5
Sequence 5, Application US/10689576
GENERAL INFORMATION:
APPLICANT: Aleesi, Dario R
TITLE OF INVENTION: ENZYME
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jaekie Fleischmann & Muel, LLP
STREET: 39 State Street
CITY: Rochester
STATE: New York
COUNTRY: USA
ZIP: 14614-1310
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/689,576
FILING DATE: 20-Oct-2003
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/943,667
FILING DATE: 03-OCT-1997
APPLICATION NUMBER: GB 9705462.1
FILING DATE: 17-MAR-1997
APPLICATION NUMBER: GB 9712826.8
FILING DATE: 19-JUN-1997
APPLICATION NUMBER: GB 9717253.0
FILING DATE: 15-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: Braman, Susan J
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 87792.97R421
TELECOMMUNICATION INFORMATION:
TELEPHONE: 716-262-3640
TELEFAX: 716-262-4133
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal

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SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-689-576-5

Query Match 100.0%; Score 46; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDHPFFVK 8
Db 1 LDHPFFVK 8

RESULT 2
US-10-689-576-1
Sequence 1, Application US/10689576
GENERAL INFORMATION:
APPLICANT: Aleesi, Dario R
TITLE OF INVENTION: ENZYME
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jaackie Fleischmann & Muegel, LLP
STREET: 39 State Street
CITY: Rochester
STATE: New York
COUNTRY: USA
ZIP: 14614-1310
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/689,576
FILING DATE: 20-Oct-2003
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/943,667
FILING DATE: 03-Oct-1997
APPLICATION NUMBER: GB 9705462.1
FILING DATE: 17-MAR-1997
APPLICATION NUMBER: GB 9712826.8
FILING DATE: 19-JUN-1997
APPLICATION NUMBER: GB 9717253.0
FILING DATE: 15-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: Braham, Susan J
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 87792.97R421
TELECOMMUNICATION INFORMATION:
TELEPHONE: 716-262-3640
TELEFAX: 716-262-4133
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 556 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-689-576-1

Query Match 100.0%; Score 46; DB 1; Length 556;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LDHPFFVK 8
Db 137 LDHPFFVK 144

RESULT 3
US-10-689-576-4
Sequence 4, Application US/10689576
GENERAL INFORMATION:
APPLICANT: Aleesi, Dario R
TITLE OF INVENTION: ENZYME
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jaackie Fleischmann & Muegel, LLP
STREET: 39 State Street
CITY: Rochester
STATE: New York
COUNTRY: USA
ZIP: 14614-1310
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/689,576
FILING DATE: 20-Oct-2003
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/943,667
FILING DATE: 03-Oct-1997
APPLICATION NUMBER: GB 9705462.1
FILING DATE: 17-MAR-1997
APPLICATION NUMBER: GB 9712826.8
FILING DATE: 19-JUN-1997
APPLICATION NUMBER: GB 9717253.0
FILING DATE: 15-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: Braham, Susan J
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 87792.97R421
TELECOMMUNICATION INFORMATION:
TELEPHONE: 716-262-3640
TELEFAX: 716-262-4133
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-689-576-4

Query Match 21.7%; Score 10; DB 1; Length 10;
Best Local Similarity 28.6%; Pred. No. 0;
Matches 2; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 DHPEFVK 8
Db 4 EYLIFK 10

RESULT 4
US-10-689-576-3
Sequence 3, Application US/10689576
GENERAL INFORMATION:
APPLICANT: Aleesi, Dario R
TITLE OF INVENTION: ENZYME
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jaackie Fleischmann & Muegel, LLP
STREET: 39 State Street
CITY: Rochester

STATE: New York
 COUNTRY: USA
 ZIP: 14614-1310
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/689,576
 FILING DATE: 20-Oct-2003
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/943,667
 FILING DATE: 03-Oct-1997
 APPLICATION NUMBER: GB 9705462.1
 FILING DATE: 17-MAR-1997
 APPLICATION NUMBER: GB 9712826.8
 FILING DATE: 19-JUN-1997
 APPLICATION NUMBER: GB 9717253.0
 FILING DATE: 15-AUG-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Braham, Susan J
 REGISTRATION NUMBER: 34,103
 REFERENCE/DOCKET NUMBER: 87792.97R421
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 716-262-3640
 TELEFAX: 716-262-4133
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 16 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FRAGMENT TYPE: internal
 SEQUENCE DESCRIPTION: SEQ ID NO: 3:
 US-10-689-576-3

Query Match 21.7% Score 10; DB 1; Length 16;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 FV 7
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 Db 4 FV 5

Search completed: May 17, 2006, 13:06:00
 Job time : 0.001 secs

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GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 16, 2006, 13:40:29 ; Search time 27 Seconds
(without alignments)
27.822 Million cell updates/sec

Title: US-10-689-576-3

Perfect score: 79

Sequence: 1 ANSFVGTAAQVSPRL 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 250354 seqs, 46948837 residues

Total number of hits satisfying chosen parameters: 250354

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications MA New:*
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2: /SIDS5/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
3: /SIDS5/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
4: /SIDS5/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
5: /SIDS5/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
6: /SIDS5/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
7: /SIDS5/ptodata/2/pubpaa/US09_NEW_PUB.pep1.*
8: /SIDS5/ptodata/2/pubpaa/US10_NEW_PUB.pep1.*
9: /SIDS5/ptodata/2/pubpaa/US10_NEW_PUB.pep1.*
10: /SIDS5/ptodata/2/pubpaa/US11_NEW_PUB.pep1.*
11: /SIDS5/ptodata/2/pubpaa/US11_NEW_PUB.pep1.*
12: /SIDS5/ptodata/2/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	60	75.9	393	8 US-10-511-814-19	Sequence 19, Appl
2	60	75.9	393	8 US-10-511-814-20	Sequence 20, Appl
3	60	75.9	393	8 US-10-511-814-21	Sequence 21, Appl
4	60	75.9	393	11 US-11-111-239-11	Sequence 11, Appl
5	60	75.9	428	11 US-11-188-298-22499	Sequence 22499, A
6	60	75.9	443	11 US-11-188-298-3245	Sequence 3245, Ap
7	60	75.9	686	11 US-11-096-568A-14747	Sequence 14747, A
8	60	75.9	749	11 US-11-087-099-6685	Sequence 6685, Ap
9	60	75.9	749	11 US-11-188-298-17142	Sequence 17142, A
10	60	75.9	750	11 US-11-087-099-5543	Sequence 5543, Ap
11	60	75.9	750	11 US-11-188-298-16098	Sequence 16098, A
12	60	75.9	761	11 US-11-096-568A-14746	Sequence 14746, A
13	60	75.9	911	11 US-11-096-568A-14745	Sequence 14745, A
14	60	75.9	921	11 US-11-188-298-21552	Sequence 21552, A
15	60	75.9	923	11 US-11-188-298-9370	Sequence 9370, Ap
16	60	75.9	927	11 US-11-188-298-9708	Sequence 9708, Ap
17	60	75.9	963	11 US-11-188-298-15124	Sequence 15124, A
18	60	75.9	970	11 US-11-188-298-8880	Sequence 8880, Ap
19	60	75.9	976	11 US-11-188-298-1147	Sequence 1147, Ap
20	60	75.9	976	11 US-11-188-298-15203	Sequence 15203, A
21	60	75.9	1465	11 US-11-087-099-1792	Sequence 1792, Ap

22	60	75.9	1465	11 US-11-087-099-10059	Sequence 10059, A
23	60	75.9	1465	11 US-11-188-298-1786	Sequence 1786, Ap
24	60	75.9	1465	11 US-11-188-298-20298	Sequence 20298, A
25	59	74.7	1019	11 US-11-188-298-3587	Sequence 3587, Ap
26	58	73.4	526	11 US-11-087-099-6670	Sequence 6670, Ap
27	58	73.4	566	11 US-11-087-099-9603	Sequence 9603, Ap
28	58	73.4	623	11 US-11-087-099-495	Sequence 495, Appl
29	58	73.4	756	11 US-11-222-158-2	Sequence 2, Appl
30	58	73.4	1092	11 US-11-087-099-6350	Sequence 6350, Ap
31	58	73.4	1092	11 US-11-188-298-5787	Sequence 5787, Ap
32	57	72.2	400	11 US-11-111-239-12	Sequence 12, Appl
33	57	72.2	458	11 US-11-087-099-10379	Sequence 10379, A
34	57	72.2	554	11 US-11-087-099-3239	Sequence 3239, Ap
35	57	72.2	557	11 US-11-087-099-8936	Sequence 8936, Ap
36	57	72.2	791	11 US-11-087-099-7833	Sequence 7833, Ap
37	57	72.2	799	11 US-11-087-099-9393	Sequence 9393, Ap
38	57	72.2	800	11 US-11-087-099-8511	Sequence 8511, Ap
39	57	72.2	926	11 US-11-087-099-345	Sequence 345, Appl
40	56	70.9	462	11 US-11-087-099-3746	Sequence 3746, Ap
41	54	68.4	745	9 US-10-995-561-659	Sequence 659, Appl
42	54	68.4	745	11 US-11-109-156-14	Sequence 14, Appl
43	54	68.4	745	11 US-11-222-158-4	Sequence 4, Appl
44	53	67.1	118	11 US-11-087-099-2183	Sequence 2183, Ap
45	53	67.1	417	11 US-11-096-568A-31333	Sequence 31333, A

ALIGNMENTS

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RESULT 1
US-10-511-814-19
Sequence 19, Application US/10511814
; Publication No. US20060088472A1
; GENERAL INFORMATION:
; APPLICANT: McCance, Dennis
; TITLE OF INVENTION: ET REGULATION OF P21 (CIP1) THROUGH AKT
; FILE REFERENCE: 21108.001602
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US03/12667
; PRIOR FILING DATE: 2003-04-21
; PRIOR APPLICATION NUMBER: 60/374,245
; PRIOR FILING DATE: 2002-04-19
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 393
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/Note =
US-10-511-814-19
Query Match 75.9%; Score 60; DB 8; Length 393;
Beet local similarity 75.0%; Pred. No. 0.0041;
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
Cy 1 ANSFVGTAAQVSPRL 16
Db 220 ANSFVGTAAQVSPRL 235
RESULT 2
US-10-511-814-20
Sequence 20, Application US/10511814
; Publication No. US20060088472A1
; GENERAL INFORMATION:
; APPLICANT: McCance, Dennis
; TITLE OF INVENTION: ET REGULATION OF P21 (CIP1) THROUGH AKT
; FILE REFERENCE: 21108.001602
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CURRENT APPLICATION NUMBER: US/10/511,814
CURRENT FILING DATE: 2004-10-19
PRIOR APPLICATION NUMBER: PCT/US03/12667
PRIOR FILING DATE: 2003-04-21
PRIOR APPLICATION NUMBER: 60/374,245
PRIOR FILING DATE: 2002-04-19
NUMBER OF SEQ ID NOS: 21
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 20
LENGTH: 393
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:/Note =
US-10-511-814-20

Query Match 75.9%; Score 60; DB 8; Length 393;
Best Local Similarity 75.0%; Pred. No. 0.0041;
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 ANSFVGTAGYVSPRL 16
||||| :|||
Db 220 ANSFVGTSTYVSPRL 235

RESULT 3
US-10-511-814-21
Sequence 21, Application US/10511814
Publication No. US20060088472A1
GENERAL INFORMATION:
APPLICANT: McCance, Dennis
TITLE OF INVENTION: E7 REGULATION OF P21 (CIP1) THROUGH AKT
FILE REFERENCE: 21108, 001602
CURRENT APPLICATION NUMBER: US/10/511,814
CURRENT FILING DATE: 2004-10-19
PRIOR APPLICATION NUMBER: PCT/US03/12667
PRIOR FILING DATE: 2003-04-21
PRIOR APPLICATION NUMBER: 60/374,245
PRIOR FILING DATE: 2002-04-19
NUMBER OF SEQ ID NOS: 21
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 21
LENGTH: 393
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:/Note =
US-10-511-814-21

Query Match 75.9%; Score 60; DB 8; Length 393;
Best Local Similarity 75.0%; Pred. No. 0.0041;
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 ANSFVGTAGYVSPRL 16
||||| :|||
Db 220 ANSFVGTSTYVSPRL 235

RESULT 4
US-11-111-239-11
Sequence 11, Application US/11111239
Publication No. US2005027207A1
GENERAL INFORMATION:
APPLICANT: Davis, Roger J.
Ratigeaud, Joel
Gupta, Shaanil
Derijard, Benoît
TITLE OF INVENTION: CYTOKINE-, STRESS-, AND
ONCOPROTEIN-ACTIVATED HUMAN PROTEIN KINASE
KINASES

NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fieh & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/11/111,239
FILING DATE: 21-Apr-2005
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/761,569
FILING DATE: 16-Jan-2001
APPLICATION NUMBER: 09/057,009
FILING DATE: 1998-04-07
ATTORNEY/AGENT INFORMATION:
NAME: Fasse, J. Peter
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 07917/010001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 393 amino acids
TYPE: amino acid
STRANDEDNESS: Not Relevant
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-11-111-239-11

Query Match 75.9%; Score 60; DB 11; Length 393;
Best Local Similarity 75.0%; Pred. No. 0.0041;
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 ANSFVGTAGYVSPRL 16
||||| :|||
Db 220 ANSFVGTSTYVSPRL 235

RESULT 5
US-11-188-298-22499
Sequence 22499, Application US/11188298
Publication No. US20060075522A1
GENERAL INFORMATION:
APPLICANT: Abad, Mark S. et al.
TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
FILE REFERENCE: 38-21 (53452)B
CURRENT APPLICATION NUMBER: US/11/188,298
CURRENT FILING DATE: 2005-07-22
PRIOR APPLICATION NUMBER: 60/592,978
PRIOR FILING DATE: 2004-07-31
NUMBER OF SEQ ID NOS: 22569
SEQ ID NO 22499
LENGTH: 428
TYPE: PRT
ORGANISM: Pisum sativum
US-11-188-298-22499

Query Match 75.9%; Score 60; DB 11; Length 428;
Best Local Similarity 56.2%; Pred. No. 0.0045;
Matches 9; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 1 ANSFVGTAGYVSPRL 16
||||| :|||

Db 284 SNSFVGTEHYLAPELI 299

RESULT 6

US-11-188-298-3245
; Sequence 3245, Application US/11188298
; Publication No. US20060075522A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 3245
; LENGTH: 443
; TYPE: PRT
; ORGANISM: Pisum sativum
US-11-188-298-3245

Query Match 75.9%; Score 60; DB 11; Length 443;
Best Local Similarity 56.2%; Pred. No. 0.0047;
Matches 9; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 1 ANSFVGTAQYVSPELL 16
:|||||:|:|:|:
Db 295 SNSFVGTEHYLAPELI 310

RESULT 7

US-11-096-568A-14747
; Sequence 14747, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 14747
; LENGTH: 686
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(686)
; OTHER INFORMATION: Cereals Seq. ID no. 11050392
US-11-096-568A-14747

Query Match 75.9%; Score 60; DB 11; Length 686;
Best Local Similarity 56.2%; Pred. No. 0.0078;
Matches 9; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 1 ANSFVGTAQYVSPELL 16
:|||||:|:|:|:
Db 542 SNSFVGTEHYLAPELI 557

RESULT 8

US-11-087-099-6685
; Sequence 6685, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464

; SEQ ID NO 6685
; LENGTH: 749
; TYPE: PRT
; ORGANISM: Chlamydomonas reinhardtii
US-11-087-099-6685

Query Match 75.9%; Score 60; DB 11; Length 749;
Best Local Similarity 62.5%; Pred. No. 0.0086;
Matches 10; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 ANSFVGTAQYVSPELL 16
:|||||:|:|:|:
Db 609 ANSFVGTEHYLAPEVI 624

RESULT 9

US-11-188-298-17142
; Sequence 17142, Application US/11188298
; Publication No. US20060075522A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 17142
; LENGTH: 749
; TYPE: PRT
; ORGANISM: Chlamydomonas reinhardtii
US-11-188-298-17142

Query Match 75.9%; Score 60; DB 11; Length 749;
Best Local Similarity 62.5%; Pred. No. 0.0086;
Matches 10; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 ANSFVGTAQYVSPELL 16
:|||||:|:|:|:
Db 609 ANSFVGTEHYLAPEVI 624

RESULT 10

US-11-087-099-5543
; Sequence 5543, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 5543
; LENGTH: 750
; TYPE: PRT
; ORGANISM: Chlamydomonas reinhardtii
US-11-087-099-5543

Query Match 75.9%; Score 60; DB 11; Length 750;
Best Local Similarity 62.5%; Pred. No. 0.0086;
Matches 10; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 ANSFVGTAQYVSPELL 16
:|||||:|:~|:|:
Db 609 ANSFVGTEHYLAPEVI 624

RESULT 11

US-11-188-298-16098
; Sequence 16098, Application US/11188298
; Publication No. US20060075522A1

```

; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 16098
; LENGTH: 750
; TYPE: PRT
; ORGANISM: Chlamydomonas reinhardtii
US-11-188-298-16098

Query Match
Best Local Similarity 75.9%; Score 60; DB 11; Length 750;
Pred. No. 0.0086;
Matches 10; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ANSFVGTQAYVSPPELL 16
Db 609 SNSFVGTEBYIAPEII 624

RESULT 12
US-11-096-568A-14746
; Sequence 14746, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 14746
; LENGTH: 761
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(761)
; OTHER INFORMATION: Ceres Seq. ID no. 11050391
US-11-096-568A-14746

Query Match
Best Local Similarity 75.9%; Score 60; DB 11; Length 761;
Pred. No. 0.0088;
Matches 9; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ANSFVGTQAYVSPPELL 16
Db 617 SNSFVGTEBYIAPEII 632

RESULT 13
US-11-096-568A-14745
; Sequence 14745, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 14745
; LENGTH: 911
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc_feature

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; LOCATION: (1)..(911)
; OTHER INFORMATION: Ceres Seq. ID no. 11050390
US-11-096-568A-14745

Query Match
Best Local Similarity 75.9%; Score 60; DB 11; Length 911;
Pred. No. 0.011;
Matches 9; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ANSFVGTQAYVSPPELL 16
Db 767 SNSFVGTEBYIAPEII 782

RESULT 14
US-11-188-298-21552
; Sequence 21552, Application US/11188298
; Publication No. US20060075522A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 21552
; LENGTH: 921
; TYPE: PRT
; ORGANISM: Oryza sativa (indica cultivar-group)
US-11-188-298-21552

Query Match
Best Local Similarity 75.9%; Score 60; DB 11; Length 921;
Pred. No. 0.011;
Matches 9; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ANSFVGTQAYVSPPELL 16
Db 778 SNSFVGTEBYIAPEII 793

RESULT 15
US-11-188-298-9370
; Sequence 9370, Application US/11188298
; Publication No. US20060075522A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 9370
; LENGTH: 923
; TYPE: PRT
; ORGANISM: Avena sativa
US-11-188-298-9370

Query Match
Best Local Similarity 75.9%; Score 60; DB 11; Length 923;
Pred. No. 0.011;
Matches 9; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ANSFVGTQAYVSPPELL 16
Db 778 SNSFVGTEBYIAPEII 793

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Search completed: May 16, 2006, 13:43:36
Job time : 28 secs

9

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OM protein - protein search, using sw model

Run on: May 17, 2006, 11:56:25 ; Search time 180 Seconds
(without alignments)
41.175 Million cell updates/sec

Title: US-10-689-576-3

Perfect score: 79

Sequence: 1 ANSRVGTATQYVSPPELL 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:*
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2: /EMC_Celerra_SIDS3/prodata/2/pubpaa/US08_PUBCOMB.pep:*
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5: /EMC_Celerra_SIDS3/prodata/2/pubpaa/US10B_PUBCOMB.pep:*
6: /EMC_Celerra_SIDS3/prodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	79	100.0	16	4 US-10-190-012-3	Sequence 3, Appli
2	79	100.0	16	5 US-10-689-576-3	Sequence 30, Appli
3	79	100.0	19	5 US-10-862-195-30	Sequence 1378, Ap
4	79	100.0	19	5 US-10-862-195-1378	Sequence 185, App
5	79	100.0	25	3 US-09-205-658-185	Sequence 185, App
6	79	100.0	25	3 US-09-963-693-185	Sequence 196, App
7	79	100.0	98	3 US-09-205-658-196	Sequence 196, App
8	79	100.0	98	3 US-09-963-693-196	Sequence 13, Appl
9	79	100.0	285	4 US-10-217-574-13	Sequence 1375, Ap
10	79	100.0	285	4 US-10-217-555-13	Sequence 1375, Ap
11	79	100.0	319	5 US-10-473-127-1375	Sequence 1366, Ap
12	79	100.0	319	5 US-10-473-127-1386	Sequence 106, App
13	79	100.0	361	4 US-10-664-421-106	Sequence 107, App
14	79	100.0	361	5 US-10-941-635-107	Sequence 1371, Ap
15	79	100.0	468	5 US-10-473-127-1371	Sequence 1385, Ap
16	79	100.0	468	5 US-10-473-127-1385	Sequence 1391, Ap
17	79	100.0	506	5 US-10-473-127-1381	Sequence 1379, Ap
18	79	100.0	535	5 US-10-473-127-1379	Sequence 245, App
19	79	100.0	556	4 US-09-771-161A-245	Sequence 1, Appli
20	79	100.0	556	4 US-10-190-012-1	Sequence 6, Appli
21	79	100.0	556	4 US-10-376-554-6	Sequence 14, Appl
22	79	100.0	556	4 US-10-704-921-14	Sequence 1372, Ap
23	79	100.0	556	5 US-10-473-127-1372	Sequence 1373, Ap
24	79	100.0	556	5 US-10-473-127-1373	Sequence 1374, Ap
25	79	100.0	556	5 US-10-473-127-1374	Sequence 1377, Ap
26	79	100.0	556	5 US-10-473-127-1377	Sequence 1378, Ap
27	79	100.0	556	5 US-10-473-127-1378	

28	79	100.0	556	5 US-10-473-127-1380	Sequence 1380, Ap
29	79	100.0	556	5 US-10-473-127-1382	Sequence 1382, Ap
30	79	100.0	556	5 US-10-473-127-1383	Sequence 1383, Ap
31	79	100.0	556	5 US-10-473-127-1384	Sequence 2053, Ap
32	79	100.0	556	5 US-10-723-860-2053	Sequence 28, Appl
33	79	100.0	556	5 US-10-689-576-1	Sequence 1331, A
34	79	100.0	556	5 US-10-509-599-28	Sequence 728, App
35	71	89.9	473	4 US-10-369-493-13231	Sequence 347, App
36	70	88.6	944	4 US-10-451-467A-728	Sequence 4163, Ap
37	69	87.3	15	4 US-10-211-088-347	Sequence 28176, A
38	68	86.1	304	4 US-10-369-493-4163	Sequence 28179, A
39	67	84.8	1081	4 US-10-451-467A-714	Sequence 133, App
40	66	83.5	539	6 US-11-097-143-28176	Sequence 29, Appl
41	66	83.5	539	6 US-11-097-143-28179	Sequence 138, App
42	66	83.5	752	4 US-10-108-605-133	
43	66	83.5	752	4 US-10-190-012-29	
44	66	83.5	752	5 US-10-689-576-29	
45	66	83.5	752	6 US-11-097-143-138	

ALIGNMENTS

RESULT 1
US-10-190-012-3
Sequence 3, Application US/10190012
Publication No. US20030108971A1
GENERAL INFORMATION:
APPLICANT: Alesei, Dario R
TITLE OF INVENTION: ENZYME
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESSES:
ADDRESSER: Jaackle Fleischmann & Mugel, LLP
STREET: 39 State Street
CITY: Rochester
STATE: New York
COUNTRY: USA
ZIP: 14614-1310
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/190,012
FILING DATE: 05-Jul-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/943,667
FILING DATE: 03-Oct-1997
APPLICATION NUMBER: GB 9705462.1
FILING DATE: 17-MAR-1997
APPLICATION NUMBER: GB 9712826.8
FILING DATE: 19-JUN-1997
APPLICATION NUMBER: GB 9717253.0
FILING DATE: 15-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: Braman, Susan J
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 87792.978421
TELECOMMUNICATION INFORMATION:
TELEPHONE: 716-262-3640
TELEFAX: 716-262-4133
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULAR TYPE: peptide
HYPOTHEetical: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal

SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-190-012-3

Query Match 100.0%; Score 79; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.5e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ANSFVGTAGYVSPFL 16
Db 1 ANSFVGTAGYVSPFL 16

RESULT 2

US-10-689-576-3
Sequence 3, Application US/10689576
Publication No. US20050032185A1
GENERAL INFORMATION:
APPLICANT: Aleesi, Darlo R
TITLE OF INVENTION: ENZYME
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jaesckle Fleischmann & Muegel, LLP
STREET: 39 State Street
CITY: Rochester
STATE: New York
COUNTRY: USA
ZIP: 14614-1310
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/689, 576
FILING DATE: 20-Oct-2003
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/943, 667
FILING DATE: 03-Oct-1997
APPLICATION NUMBER: GB 9705462.1
FILING DATE: 17-MAR-1997
APPLICATION NUMBER: GB 9712826.8
FILING DATE: 19-JUN-1997
APPLICATION NUMBER: GB 9717253.0
FILING DATE: 15-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: Brian, Susan J
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 87792, 97R421
TELECOMMUNICATION INFORMATION:
TELEPHONE: 716-262-3640
TELEFAX: 716-262-4133
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-689-576-3

Query Match 100.0%; Score 79; DB 5; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.5e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ANSFVGTAGYVSPFL 16
Db 1 ANSFVGTAGYVSPFL 16

RESULT 3

US-10-862-195-30
Sequence 30, Application US/10862195
Publication No. US20050164324A1
GENERAL INFORMATION:
APPLICANT: CYCIG, STEVEN P.
TITLE OF INVENTION: SYSTEMS, METHODS AND KITS FOR CHARACTERIZING PHOSPHOPROTEOMES
FILE REFERENCE: 58890(70207)
CURRENT APPLICATION NUMBER: US/10/862,195
CURRENT FILING DATE: 2004-06-04
PRIOR FILING DATE: 2003-06-04
NUMBER OF SEQ ID NOS: 2245
SOFTWARE: Patent In version 3.2
SEQ ID NO 30
LENGTH: 19
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: See specification as filed for preferred embodiments
OTHER INFORMATION: and description of phosphorylation sites
US-10-862-195-30

Query Match 100.0%; Score 79; DB 5; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.8e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ANSFVGTAGYVSPFL 16
Db 1 ANSFVGTAGYVSPFL 16

RESULT 4

US-10-862-195-1378
Sequence 1378, Application US/10862195
Publication No. US20050164324A1
GENERAL INFORMATION:
APPLICANT: CYCIG, STEVEN P.
TITLE OF INVENTION: SYSTEMS, METHODS AND KITS FOR CHARACTERIZING PHOSPHOPROTEOMES
FILE REFERENCE: 58890(70207)
CURRENT APPLICATION NUMBER: US/10/862,195
CURRENT FILING DATE: 2004-06-04
PRIOR APPLICATION NUMBER: 60/476,010
PRIOR FILING DATE: 2003-06-04
NUMBER OF SEQ ID NOS: 2245
SOFTWARE: Patent In version 3.2
SEQ ID NO 1378
LENGTH: 19
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: See specification as filed for preferred embodiments
OTHER INFORMATION: and description of phosphorylation sites
US-10-862-195-1378

Query Match 100.0%; Score 79; DB 5; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.8e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ANSFVGTAGYVSPFL 16
Db 1 ANSFVGTAGYVSPFL 16

RESULT 5

US-09-205-658-185
Sequence 185, Application US/09205658
Patent No. US20010029617A1
GENERAL INFORMATION:
APPLICANT: Ruvkun, Gary
APPLICANT: Ogg, Scott
TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR

```

; TITLE OF INVENTION: IMPAIRED GLUCOSE TOLERANCE CONDITIONS
; FILE REFERENCE: 00786/351004
; CURRENT APPLICATION NUMBER: US/09/205,658
; CURRENT FILING DATE: 1998-12-03
; EARLIER APPLICATION NUMBER: 08/857,076
; EARLIER FILING DATE: 1997-05-15
; EARLIER APPLICATION NUMBER: 08/888,534
; EARLIER FILING DATE: 1997-07-07
; EARLIER APPLICATION NUMBER: US98/10080
; EARLIER FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 328
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 185
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Mus musculus or Homo sapiens
US-09-205-658-185

Query Match          100.0%; Score 79; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 2,4e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ANSFVGTAGYVSPELL 16
        |||||
Db      8 ANSFVGTAGYVSPELL 23

RESULT 6
US-09-963-693-185
; Sequence 185, Application US/09963693
; Publication No. US20030181364A1
; GENERAL INFORMATION:
; APPLICANT: Ruvkun, Gary
; APPLICANT: Ogg, Scott
; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR
; TITLE OF INVENTION: IMPAIRED GLUCOSE TOLERANCE CONDITIONS
; FILE REFERENCE: 00786/351004
; CURRENT APPLICATION NUMBER: US/09/963,693
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/205,658
; PRIOR FILING DATE: 1998-12-03
; PRIOR APPLICATION NUMBER: 08/857,076
; PRIOR FILING DATE: 1997-05-15
; PRIOR APPLICATION NUMBER: 08/888,534
; PRIOR FILING DATE: 1997-07-07
; PRIOR APPLICATION NUMBER: US98/10080
; PRIOR FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 328
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 185
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Mus musculus or Homo sapiens
US-09-963-693-185

Query Match          100.0%; Score 79; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 2,4e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ANSFVGTAGYVSPELL 16
        |||||
Db      8 ANSFVGTAGYVSPELL 23

RESULT 7
US-09-205-658-196
; Sequence 196, Application US/09205658
; Patent No. US20010029617A1
; GENERAL INFORMATION:
; APPLICANT: Ruvkun, Gary
; APPLICANT: Ogg, Scott
; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR
; TITLE OF INVENTION: IMPAIRED GLUCOSE TOLERANCE CONDITIONS
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; FILE REFERENCE: 00786/351004
; CURRENT APPLICATION NUMBER: US/09/205,658
; CURRENT FILING DATE: 1998-12-03
; EARLIER APPLICATION NUMBER: 08/857,076
; EARLIER FILING DATE: 1997-05-15
; EARLIER APPLICATION NUMBER: 08/888,534
; EARLIER FILING DATE: 1997-07-07
; EARLIER APPLICATION NUMBER: US98/10080
; EARLIER FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 328
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 196
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-205-658-196

Query Match          100.0%; Score 79; DB 3; Length 98;
Best Local Similarity 100.0%; Pred. No. 1e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ANSFVGTAGYVSPELL 16
        |||||
Db      7 ANSFVGTAGYVSPELL 22

RESULT 8
US-09-963-693-196
; Sequence 196, Application US/09963693
; Publication No. US20030181364A1
; GENERAL INFORMATION:
; APPLICANT: Ruvkun, Gary
; APPLICANT: Ogg, Scott
; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR
; TITLE OF INVENTION: IMPAIRED GLUCOSE TOLERANCE CONDITIONS
; FILE REFERENCE: 00786/351004
; CURRENT APPLICATION NUMBER: US/09/963,693
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/205,658
; PRIOR FILING DATE: 1998-12-03
; PRIOR APPLICATION NUMBER: 08/857,076
; PRIOR FILING DATE: 1997-05-15
; PRIOR APPLICATION NUMBER: 08/888,534
; PRIOR FILING DATE: 1997-07-07
; PRIOR APPLICATION NUMBER: US98/10080
; PRIOR FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 328
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 196
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-963-693-196

Query Match          100.0%; Score 79; DB 3; Length 98;
Best Local Similarity 100.0%; Pred. No. 1e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ANSFVGTAGYVSPELL 16
        |||||
Db      7 ANSFVGTAGYVSPELL 22

RESULT 9
US-10-217-574-13
; Sequence 13, Application US/10217574
; Publication No. US20040005687A1
; GENERAL INFORMATION:
; APPLICANT: Barford, David
; APPLICANT: Yang, Jing
; APPLICANT: Hemmings, Brian A
; APPLICANT: Cron, Peter D
; TITLE OF INVENTION: Kinase Crystal Structures
```

```
; FILE REFERENCE: 44237
; CURRENT APPLICATION NUMBER: US/10/217,574
; CURRENT FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: GB 0119860.5
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: GB 0209985.1
; PRIOR FILING DATE: 2002-05-01
; PRIOR APPLICATION NUMBER: GB 0216215.4
; PRIOR FILING DATE: 2002-07-12
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 285
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Sequence source
; OTHER INFORMATION: uncertain
US-10-217-574-13
```

```
Query Match      100.0%; Score 79; DB 4; Length 285;
Best Local Similarity 100.0%; Pred. No. 3.3e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 ANSFVGTAAQYVSPDLL 16
Db      164 ANSFVGTAAQYVSPDLL 179
```

```
RESULT 10
US-10-217-555-13
; Sequence 13, Application US/10217555
; Publication No. US2004009569A1
; GENERAL INFORMATION:
; APPLICANT: Barford, David
; APPLICANT: Yang, Jing
; APPLICANT: Hemmings, Brian A
; APPLICANT: Cron, Peter D
; TITLE OF INVENTION: Kinase Crystal Structures and Methods for
; TITLE OF INVENTION: Kinase Activation
; FILE REFERENCE: 44236
; CURRENT APPLICATION NUMBER: US/10/217,555
; CURRENT FILING DATE: 2002-12-05
; PRIOR APPLICATION NUMBER: GB 0119860.5
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: GB 0209985.1
; PRIOR FILING DATE: 2002-05-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 285
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Sequence source
; OTHER INFORMATION: uncertain
US-10-217-555-13
```

```
Query Match      100.0%; Score 79; DB 4; Length 285;
Best Local Similarity 100.0%; Pred. No. 3.3e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 ANSFVGTAAQYVSPDLL 16
Db      164 ANSFVGTAAQYVSPDLL 179
```

```
RESULT 11
US-10-473-127-1375
; Sequence 1375, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
```

```
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026WO1
; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1375
; LENGTH: 319
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-1375
```

```
Query Match      100.0%; Score 79; DB 5; Length 319;
Best Local Similarity 100.0%; Pred. No. 3.8e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 ANSFVGTAAQYVSPDLL 16
Db      2 ANSFVGTAAQYVSPDLL 17
```

```
RESULT 12
US-10-473-127-1386
; Sequence 1386, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026WO1
; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1386
; LENGTH: 319
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-1386
```

```
Query Match      100.0%; Score 79; DB 5; Length 319;
Best Local Similarity 100.0%; Pred. No. 3.8e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 ANSFVGTAAQYVSPDLL 16
Db      2 ANSFVGTAAQYVSPDLL 17
```

```
RESULT 13
```



```
US-10-664-421-106
; Sequence 106, Application US/10664421
; Publication No. US20040142864A1
; GENERAL INFORMATION:
; APPLICANT: BREMER, RYAN
; APPLICANT: IBRAHIM, PRABHA
; APPLICANT: KUMAR, ABHINAV
; APPLICANT: MANDIYAN, VALSAN
; APPLICANT: MILBURN, MICHAEL V.
; TITLE OF INVENTION: CRYSTAL STRUCTURE OF PIM-1 KINASE
; FILE REFERENCE: 039363/0703
; CURRENT APPLICATION NUMBER: US/10/664,421
; CURRENT FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: 60/412,341
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/411,398
; PRIOR FILING DATE: 2002-09-16
; NUMBER OF SEQ ID NOS: 169
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 106
; LENGTH: 361
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-664-421-106

Query Match      100.0%; Score 79; DB 4; Length 361;
Best Local Similarity 100.0%; Pred. No. 4.3e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      1 ANSFVGTAGYVSPELL 16
      |||
Db      208 ANSFVGTAGYVSPELL 223

RESULT 14
US-10-941-635-107
; Sequence 107, Application US/10941635
; Publication No. US20050164300A1
; GENERAL INFORMATION:
; APPLICANT: ARTIS, DEAN R.
; APPLICANT: BREMER, RYAN E.
; APPLICANT: GILLETTE, SAMUEL J.
; APPLICANT: HUNT, CLARENCE R.
; APPLICANT: IBRAHIM, PRABHA L.
; APPLICANT: ZUCKERMAN, REBECCA L.
; TITLE OF INVENTION: MOLECULAR SCAFFOLDS FOR KINASE LIGAND DEVELOPMENT
; FILE REFERENCE: 039363-1702
; CURRENT APPLICATION NUMBER: US/10/941,635
; CURRENT FILING DATE: 2004-09-15
; PRIOR APPLICATION NUMBER: 60/503,277
; PRIOR FILING DATE: 2003-09-15
; NUMBER OF SEQ ID NOS: 167
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 107
; LENGTH: 361
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Mammalian
; OTHER INFORMATION: protein sequence
US-10-941-635-107

Query Match      100.0%; Score 79; DB 5; Length 361;
Best Local Similarity 100.0%; Pred. No. 4.3e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      1 ANSFVGTAGYVSPELL 16
      |||
Db      208 ANSFVGTAGYVSPELL 223

RESULT 15
US-10-473-127-1371
```

```
; Sequence 1371, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W1
; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1371
; LENGTH: 468
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-1371

Query Match      100.0%; Score 79; DB 5; Length 468;
Best Local Similarity 100.0%; Pred. No. 5.7e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      1 ANSFVGTAGYVSPELL 16
      |||
Db      151 ANSFVGTAGYVSPELL 166

RESULT 16
US-10-473-127-1385
; Sequence 1385, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W1
; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1385
; LENGTH: 468
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-1385

Query Match      100.0%; Score 79; DB 5; Length 468;
Best Local Similarity 100.0%; Pred. No. 5.7e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      1 ANSFVGTAGYVSPELL 16
      |||
```

Db 151 ANSFVGTAAQYVSPPELL 166

RESULT 17
US-10-473-127-1381

; Sequence 1381, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:

; APPLICANT: Zycoos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1381
; LENGTH: 506
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-1381

Query Match 100.0%; Score 79; DB 5; Length 506;
Best Local Similarity 100.0%; Pred. No. 6,2e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ANSFVGTAAQYVSPPELL 16
Db 189 ANSFVGTAAQYVSPPELL 204

RESULT 18

US-10-473-127-1379
; Sequence 1379, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycoos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1379
; LENGTH: 535
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-1379

Query Match 100.0%; Score 79; DB 5; Length 535;

Best Local Similarity 100.0%; Pred. No. 6,6e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ANSFVGTAAQYVSPPELL 16
Db 218 ANSFVGTAAQYVSPPELL 233

RESULT 19

US-09-771-161A-245
; Sequence 245, Application US/09771161A
; Patent No. US20020110811A1
; GENERAL INFORMATION:
; APPLICANT: LEVINE, et al.
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
; FILE REFERENCE: 802620-2005.1
; CURRENT APPLICATION NUMBER: US/09/771,161A
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/724,676
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 136776
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 135619
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 245
; LENGTH: 556
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-771-161A-245

Query Match 100.0%; Score 79; DB 3; Length 556;
Best Local Similarity 100.0%; Pred. No. 6,9e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ANSFVGTAAQYVSPPELL 16
Db 239 ANSFVGTAAQYVSPPELL 254

RESULT 20

US-10-190-012-1
; Sequence 1, Application US/10190012
; Publication No. US20030108971A1
; GENERAL INFORMATION:
; APPLICANT: Aleesi, Darío R
; TITLE OF INVENTION: ENZYME
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jaeckle Fleischmann & Mugel, LLP
; STREET: 39 State Street
; CITY: Rochester
; STATE: New York
; COUNTRY: USA
; ZIP: 14614-1310
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/190,012
; FILING DATE: 05-Jul-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/943,667
; FILING DATE: 03-Oct-1997
; APPLICATION NUMBER: GB 9705462.1
; FILING DATE: 17-MAR-1997
; APPLICATION NUMBER: GB 9712826.8
; FILING DATE: 19-JUN-1997
; APPLICATION NUMBER: GB 9717253.0

```
; FILING DATE: 15-AUG-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Braman, Susan J
; REGISTRATION NUMBER: 34,103
; REFERENCE/DOCKET NUMBER: 87792.97R421
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 716-262-3640
; TELEFAX: 716-262-4133
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 556 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEetical: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-190-012-1

Query Match          100.0%; Score 79; DB 4; Length 556;
Best Local Similarity 100.0%; Pred. No. 6.9e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ANSFVGTQAYVSPELL 16
        |||||||
Db      239 ANSFVGTQAYVSPELL 254

RESULT 21
US-10-376-554-6
; Sequence 6, Application US/10376554
; Publication No. US20030215849A1
; GENERAL INFORMATION:
; APPLICANT: EXELIXIS, INC.
; TITLE OF INVENTION: PPPKIE AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE
; FILE REFERENCE: EX03-017C
; CURRENT APPLICATION NUMBER: US/10/376,554
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/361,196
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 556
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-376-554-6

Query Match          100.0%; Score 79; DB 4; Length 556;
Best Local Similarity 100.0%; Pred. No. 6.9e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ANSFVGTQAYVSPELL 16
        |||||||
Db      239 ANSFVGTQAYVSPELL 254

RESULT 22
US-10-704-921-14
; Sequence 14, Application US/10704921
; Publication No. US20040166099A1
; GENERAL INFORMATION:
; APPLICANT: Rao, Patricia
; TITLE OF INVENTION: MOLECULES PREFERENTIALLY ASSOCIATED WITH EFFECTOR T CELLS
; FILE REFERENCE: TLN-026CP
; CURRENT APPLICATION NUMBER: US/10/704,921
; CURRENT FILING DATE: 2003-11-10
; PRIOR APPLICATION NUMBER: 60/467477
; PRIOR FILING DATE: 2003-05-02
```

```
; PRIOR APPLICATION NUMBER: 60/424777
; PRIOR FILING DATE: 2002-11-08
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 556
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-704-921-14

Query Match          100.0%; Score 79; DB 4; Length 556;
Best Local Similarity 100.0%; Pred. No. 6.9e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ANSFVGTQAYVSPELL 16
        |||||||
Db      239 ANSFVGTQAYVSPELL 254

RESULT 23
US-10-473-127-1372
; Sequence 1372, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1372
; LENGTH: 556
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-1372

Query Match          100.0%; Score 79; DB 5; Length 556;
Best Local Similarity 100.0%; Pred. No. 6.9e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ANSFVGTQAYVSPELL 16
        |||||||
Db      239 ANSFVGTQAYVSPELL 254

RESULT 24
US-10-473-127-1373
; Sequence 1373, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
```

```
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 1373
; LENGTH: 556
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-1373
```

```
Query Match          100.0%; Score 79; DB 5; Length 556;
Best Local Similarity 100.0%; Pred. No. 6.9e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 ANSFVGTAGYVSPELL 16
Db      239 ANSFVGTAGYVSPELL 254
```

```
RESULT 25
US-10-473-127-1374
; Sequence 1374, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 1374
; LENGTH: 556
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-1374
```

```
Query Match          100.0%; Score 79; DB 5; Length 556;
Best Local Similarity 100.0%; Pred. No. 6.9e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 ANSFVGTAGYVSPELL 16
Db      239 ANSFVGTAGYVSPELL 254
```

```
RESULT 26
US-10-473-127-1377
; Sequence 1377, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26
```

```
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 1377
; LENGTH: 556
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-1377
```

```
Query Match          100.0%; Score 79; DB 5; Length 556;
Best Local Similarity 100.0%; Pred. No. 6.9e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 ANSFVGTAGYVSPELL 16
Db      239 ANSFVGTAGYVSPELL 254
```

```
RESULT 27
US-10-473-127-1378
; Sequence 1378, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 1378
; LENGTH: 556
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-1378
```

```
Query Match          100.0%; Score 79; DB 5; Length 556;
Best Local Similarity 100.0%; Pred. No. 6.9e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 ANSFVGTAGYVSPELL 16
Db      239 ANSFVGTAGYVSPELL 254
```

```
RESULT 28
US-10-473-127-1380
; Sequence 1380, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
```

```

; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026M01
; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1380
; LENGTH: 556
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-1380
```

```

Query Match          100.0%; Score 79; DB 5; Length 556;
Best Local Similarity 100.0%; Pred. No. 6.9e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

Qy      1 ANSFVGTAGYVSPELL 16
Db      239 ANSFVGTAGYVSPELL 254
```

```

RESULT 29
US-10-473-127-1382
; Sequence 1382, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026M01
; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1382
; LENGTH: 556
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-1382
```

```

Query Match          100.0%; Score 79; DB 5; Length 556;
Best Local Similarity 100.0%; Pred. No. 6.9e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

Qy      1 ANSFVGTAGYVSPELL 16
Db      239 ANSFVGTAGYVSPELL 254
```

```

RESULT 30
US-10-473-127-1383
; Sequence 1383, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026M01
; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1383
; LENGTH: 556
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-1383
```

```

Query Match          100.0%; Score 79; DB 5; Length 556;
Best Local Similarity 100.0%; Pred. No. 6.9e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

Qy      1 ANSFVGTAGYVSPELL 16
Db      239 ANSFVGTAGYVSPELL 254
```

```

RESULT 31
US-10-473-127-1384
; Sequence 1384, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026M01
; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1384
; LENGTH: 556
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-1384
```

```

Query Match          100.0%; Score 79; DB 5; Length 556;
Best Local Similarity 100.0%; Pred. No. 6.9e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 ANSFVGTAQYVSPELL 16
Db      239 ANSFVGTAQYVSPELL 254
```

```

RESULT 32
US-10-723-860-2053
: Sequence 2053, Application US/10723860
: Publication No. US20040253606A1
: GENERAL INFORMATION:
: APPLICANT: Aziz, Nataasha
: APPLICANT: Ginsburg, Wendy M.
: APPLICANT: Zlotnik, Albert
: TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
: TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
: FILE REFERENCE: 05882.0193.NPUS01
: CURRENT APPLICATION NUMBER: US/10/723, 860
: PRIORITY FILING DATE: 2003-11-26
: PRIOR APPLICATION NUMBER: 60/429,729
: PRIOR FILING DATE: 2002-11-26
: NUMBER OF SEQ ID NOS: 8393
: SOFTWARE: PatentIn version 3.2
: SEQ ID NO 2053
: LENGTH: 556
: TYPE: PR1
: ORGANISM: Homo sapiens
US-10-723-860-2053

```

Query Match	100.0%	Score 79;	DB 5;	Length 556;
Best Local Similarity	100.0%	Pred. No. 6.9e-05;		
Matches 16;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	1	ANSFVGTAQYVSP	16
Db	239	ANSFVGTAQYVSP	254

RESULT 33
 US-10-689-576-1
 : Sequence 1, Application US/10689576
 : Publication No. US20050032185A1
 :
 : GENERAL INFORMATION:
 : APPLICANT: Aleesi, Dario R
 : TITLE OF INVENTION: ENZYME
 : NUMBER OF SEQUENCES: 35
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Ueckle Fleischmann & Muegel, LLP
 : STREET: 39 State Street
 : CITY: Rochester
 : STATE: New York
 : COUNTRY: USA
 : ZIP: 14614-1110
 :
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: Patent in Releasee #1.0, Version #1.30
 :
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/10/689,576
 : FILING DATE: 20-Oct-2003
 : CLASSIFICATION: 435
 :
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: US/08/943,667
 : FILING DATE: 03-Oct-1997
 : APPLICATION NUMBER: GB 9705462.1
 : FILING DATE: 17-MAR-1997
 : APPLICATION NUMBER: GB 9712826.8
 : FILING DATE: 19-JUN-1997
 : APPLICATION NUMBER: GB 9717253.0
 : FILING DATE: 15-AUG-1997
 :
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Briaman, Susan J
 : REGISTRATION NUMBER: 34,103

```

? REFERENCE/DOCKET NUMBER: 87792.97R421
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 716-262-3640
? TELEFAX: 716-262-4113
? INFORMATION FOR SEQ ID NO: 1:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 556 amino acids
? TYPE: amino acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: protein
? HYPOTHEICAL: NO
? ANTI-SENSE: NO
? ORIGINAL SOURCE:
? ORGANISM: Homo sapiens
? SQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-689-576-1

```

Query Match	100.0%;	Score 79;	DB 5;	Length 556;
Best Local Similarity	100.0%;	Pred. No. 6.9e-05;		
Matches 16;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

```
QY      1 ANSFVGTAQYVSPELL 16
          |||||
Db      239 ANSFVGTAQYVSPELL 254
```

```

RESULT 34
US-10-509-599-28
? Sequence 28, Application US/10509599
? Publication No. US20050216961A1
? GENERAL INFORMATION:
? APPLICANT: Delaney, Allen
? TITLE OF INVENTION: Cancer Associated Protein Kinases and their Uses
? FILE REFERENCE: SMAR-043
? CURRENT APPLICATION NUMBER: US/10/509,599
? CURRENT FILING DATE: 2004-09-28
? PRIOR APPLICATION NUMBER: 60/368,853
? PRIOR FILING DATE: 2002-03-28
? PRIOR APPLICATION NUMBER: PCT/CA03/00409
? PRIOR FILING DATE: 2003-03-21
? NUMBER OF SEQ ID NOS: 28
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 28
? LENGTH: 556
? TYPE: PRT
? ORGANISM: Homo sapiens
? FEATURE:
? NAME/KEY: UNSURE
? LOCATION: (0)...(0)
? OTHER INFORMATION: PDPK1 kinase polypeptide
US-10-509-599-28

```

Query Match	100.0%	Score 79	DB 5	Length 556
Best Local Similarity	100.0%	Pred. No. 6.9e-05		
Matches	16	Conservative	0	Mismatches 0
				Indels 0
				Gaps 0

QY	1	ANSFVGTAQYVSP	16
Db	239	ANSFVGTAQYVSP	254

```

RESULT 35
US-10-369-493-13231
; Sequence 13231, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF

```

```
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; PRIOR FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 13231
; LENGTH: 473
; TYPE: PRT
; ORGANISM: Aspergillus nidulans
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(473)
; OTHER INFORMATION: unsure at all Xaa locations
US-10-369-493-13231

Query Match          89.9%; Score 71; DB 4; Length 473;
Best Local Similarity 87.5%; Pred. No. 0.0014;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 ANSFVGTAGYVSPELL 16
       |||:|||||:|||||
DB      238 ASFFVGTAEYVSPELL 253

RESULT 36
US-10-451-467A-728
; Sequence 728, Application US/10451467A
; Publication No. US20040161840A1
; GENERAL INFORMATION:
; APPLICANT: CONTRERAS, ROLAND HENRI
; APPLICANT: EBERHARDT, INES
; APPLICANT: LUYTEN, WALTER HERMAN MARIA LOUIS
; APPLICANT: REEMANS, RIEKA JOSEPHINA
; TITLE OF INVENTION: BAX-RESPONSIVE GENES FOR DRUG TARGET IDENTIFICATION IN
; TITLE OF INVENTION: YEAST AND FUNGI
; FILE REFERENCE: JAB-1667
; CURRENT APPLICATION NUMBER: US/10/451,467A
; CURRENT FILING DATE: 2003-06-19
; PRIOR APPLICATION NUMBER: EP 00870318.3
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: EP 01870002.1
; PRIOR FILING DATE: 2001-01-04
; PRIOR APPLICATION NUMBER: EP 01870003.9
; PRIOR FILING DATE: 2001-01-09
; NUMBER OF SEQ ID NOS: 732
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 728
; LENGTH: 944
; TYPE: PRT
; ORGANISM: Candida albicans
US-10-451-467A-728

Query Match          88.6%; Score 70; DB 4; Length 944;
Best Local Similarity 87.5%; Pred. No. 0.0044;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 ANSFVGTAGYVSPELL 16
       |||:|||||:|||||
DB      405 AKSFVGTAEYVSPELL 420

RESULT 37
US-10-211-088-347
; Sequence 347, Application US/10211088
; Publication No. US20030104479A1
; GENERAL INFORMATION:
; APPLICANT: BRIGHT, GARY R.
; APPLICANT: PREMKUMAR, D. DAVID
; APPLICANT: CHEN, YIH-TAI
; TITLE OF INVENTION: NO-US20030104479A1el Fusion Proteins And Assays For Molecular Bi
; FILE REFERENCE: 01-1022-US
```

```
; CURRENT APPLICATION NUMBER: US/10/211,088
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/309,395
; PRIOR FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/341,589
; PRIOR FILING DATE: 2001-12-13
; NUMBER OF SEQ ID NOS: 366
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 347
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Post-translational modification site
US-10-211-088-347

Query Match          87.3%; Score 69; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.5e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 SFVGTAGYVSPELL 16
       |||:|||||:|||||
DB      1 SFVGTAGYVSPELL 14

RESULT 38
US-10-369-493-4163
; Sequence 4163, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: CAO, YONGWEI
; APPLICANT: HINKLE, GREGORY J.
; APPLICANT: SLATER, STEVEN C.
; APPLICANT: GOLDMAN, BARRY S.
; APPLICANT: CHEN, XIANFENG
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 4163
; LENGTH: 304
; TYPE: PRT
; ORGANISM: Neurospora crassa
US-10-369-493-4163

Query Match          86.1%; Score 68; DB 4; Length 304;
Best Local Similarity 87.5%; Pred. No. 0.0029;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 ANSFVGTAGYVSPELL 16
       |||:|||||:|||||
DB      179 AASFVGTAEYVSPELL 194

RESULT 39
US-10-451-467A-714
; Sequence 714, Application US/10451467A
; Publication No. US20040161840A1
; GENERAL INFORMATION:
; APPLICANT: CONTRERAS, ROLAND HENRI
; APPLICANT: EBERHARDT, INES
; APPLICANT: LUYTEN, WALTER HERMAN MARIA LOUIS
; APPLICANT: REEMANS, RIEKA JOSEPHINA
; TITLE OF INVENTION: BAX-RESPONSIVE GENES FOR DRUG TARGET IDENTIFICATION IN
; TITLE OF INVENTION: YEAST AND FUNGI
; FILE REFERENCE: JAB-1667
; CURRENT APPLICATION NUMBER: US/10/451,467A
; CURRENT FILING DATE: 2003-06-19
; PRIOR APPLICATION NUMBER: EP 00870318.3
```

;; PRIOR FILING DATE: 2000-12-22
;; PRIOR APPLICATION NUMBER: EP 01870002.1
;; PRIOR FILING DATE: 2001-01-04
;; PRIOR APPLICATION NUMBER: EP 01870003.9
;; PRIOR FILING DATE: 2001-01-09
;; NUMBER OF SEQ ID NOS: 732
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 714
;; LENGTH: 1081
;; TYPE: PRT
;; ORGANISM: Saccharomyces cerevisiae
US-10-451-467A-714

Query March 84.8%; Score 67; DB 4; Length 1081;
Best Local Similarity 81.2%; Pred. No. 0.017;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 SFVGTAGYVSPPELL 16
Db 346 SKSFVGTAEVSPPELL 361

RESULT 40
US-11-097-143-28176
;; Sequence 28176, Application US/11097143
;; Publication No. US20050208558A1
;; GENERAL INFORMATION:
;; APPLICANT: Venter, J. Craig
;; APPLICANT: et al.
;; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
;; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
;; FILE REFERENCE: CLO00728
;; CURRENT APPLICATION NUMBER: US/11/097,143
;; PRIOR FILING DATE: 2005-04-04
;; PRIOR APPLICATION NUMBER: 60/157,832
;; PRIOR FILING DATE: 1999-10-05
;; PRIOR APPLICATION NUMBER: 60/160,191
;; PRIOR FILING DATE: 1999-10-19
;; PRIOR APPLICATION NUMBER: 60/161,932
;; PRIOR FILING DATE: 1999-10-28
;; PRIOR APPLICATION NUMBER: 60/164,769
;; PRIOR FILING DATE: 1999-11-12
;; PRIOR APPLICATION NUMBER: 60/173,383
;; PRIOR FILING DATE: 1999-12-28
;; PRIOR APPLICATION NUMBER: 60/175,693
;; PRIOR FILING DATE: 2000-01-12
;; PRIOR APPLICATION NUMBER: 60/184,831
;; PRIOR FILING DATE: 2000-02-24
;; PRIOR APPLICATION NUMBER: 60/191,637
;; NUMBER OF SEQ ID NOS: 43008
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 28176
;; LENGTH: 539
;; TYPE: PRT
;; ORGANISM: DROSOPHILA
US-11-097-143-28176

;; ORGANISM: DROSOPHILA
US-11-097-143-28176

Query March 83.5%; Score 66; DB 6; Length 539;
Best Local Similarity 92.9%; Pred. No. 0.012;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 SFVGTAGYVSPPELL 16
Db 172 SFVGTAGYVSPPEVL 185

RESULT 41
US-11-097-143-28179
;; Sequence 28179, Application US/11097143
;; Publication No. US20050208558A1
;; GENERAL INFORMATION:

;; APPLICANT: Venter, J. Craig
;; APPLICANT: et al.
;; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
;; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
;; FILE REFERENCE: CLO00728
;; CURRENT APPLICATION NUMBER: US/11/097,143
;; PRIOR FILING DATE: 2005-04-04
;; PRIOR APPLICATION NUMBER: 60/157,832
;; PRIOR FILING DATE: 1999-10-05
;; PRIOR APPLICATION NUMBER: 60/160,191
;; PRIOR FILING DATE: 1999-10-19
;; PRIOR APPLICATION NUMBER: 60/161,932
;; PRIOR FILING DATE: 1999-10-28
;; PRIOR APPLICATION NUMBER: 60/164,769
;; PRIOR FILING DATE: 1999-11-12
;; PRIOR APPLICATION NUMBER: 60/173,383
;; PRIOR FILING DATE: 1999-12-28
;; PRIOR APPLICATION NUMBER: 60/175,693
;; PRIOR FILING DATE: 2000-01-12
;; PRIOR APPLICATION NUMBER: 60/184,831
;; PRIOR FILING DATE: 2000-02-24
;; PRIOR APPLICATION NUMBER: 60/191,637
;; PRIOR FILING DATE: 2000-03-23
;; NUMBER OF SEQ ID NOS: 43008
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 28179
;; LENGTH: 539
;; TYPE: PRT
;; ORGANISM: DROSOPHILA
US-11-097-143-28179

Query March 83.5%; Score 66; DB 6; Length 539;
Best Local Similarity 92.9%; Pred. No. 0.012;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 SFVGTAGYVSPPELL 16
Db 172 SFVGTAGYVSPPEVL 185

RESULT 42
US-10-108-605-133
;; Sequence 133, Application US/10108605
;; Publication No. US20020160934A1
;; GENERAL INFORMATION:
;; APPLICANT: Broadus, Julie
;; APPLICANT: Stam, Lynn
;; APPLICANT: Bachmann, Jane
;; APPLICANT: Kamdar, Kim
;; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FROM DROSOPHILA MELANOGASTER THAT ENCODE
;; TITLE OF INVENTION: PROTEINS ESSENTIAL FOR LARVAL VIABILITY AND USES THEREOF
;; FILE REFERENCE: 31133B
;; CURRENT APPLICATION NUMBER: US/10/108,605
;; PRIOR FILING DATE: 2002-03-27
;; PRIOR APPLICATION NUMBER: US 09/761,142
;; PRIOR FILING DATE: 2001-01-16
;; PRIOR APPLICATION NUMBER: US 60/176,418
;; PRIOR FILING DATE: 2000-01-14
;; NUMBER OF SEQ ID NOS: 361
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 133
;; LENGTH: 752
;; TYPE: PRT
;; ORGANISM: Drosophila melanogaster
US-10-108-605-133

Query March 83.5%; Score 66; DB 4; Length 752;
Best Local Similarity 92.9%; Pred. No. 0.017;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 SFVGTAGYVSPPELL 16
Db 172 SFVGTAGYVSPPEVL 185

Db 385 SFVGTAGYVSPEVL 398

RESULT 43

US-10-190-012-29

; Sequence 29, Application US/10190012
; Publication No. US20030108971A1

GENERAL INFORMATION:

APPLICANT: Aleasi, Dario R

TITLE OF INVENTION: ENZYME

NUMBER OF SEQUENCES: 35

CORRESPONDENCE ADDRESS:

ADDRESSEE: Jaackle Fleischmann & Muegel, LLP

STREET: 39 State Street

CITY: Rochester

STATE: New York

COUNTRY: USA

ZIP: 14614-1310

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/190,012

FILING DATE: 05-JUL-2002

CLASSIFICATION: <unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/943,667

FILING DATE: 03-OCT-1997

APPLICATION NUMBER: GB 9705462.1

FILING DATE: 17-MAR-1997

APPLICATION NUMBER: GB 9712826.8

FILING DATE: 19-JUN-1997

APPLICATION NUMBER: GB 9717253.0

FILING DATE: 15-AUG-1997

ATTORNEY/AGENT INFORMATION:

NAME: Braham, Susan J

REGISTRATION NUMBER: 34,103

REFERENCE/DOCKET NUMBER: 87792.97R421

TELECOMMUNICATION INFORMATION:

TELEPHONE: 716-262-3640

TELEFAX: 716-262-4133

INFORMATION FOR SEQ ID NO: 29:

SEQUENCE CHARACTERISTICS:

LENGTH: 752 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: Drosophila

SEQUENCE DESCRIPTION: SEQ ID NO: 29:

US-10-190-012-29

Query Match 83.5%; Score 66; DB 4; Length 752;

Best Local Similarity 92.9%; Pred. No. 0.017;

Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 SFVGTAGYVSPEVL 16

Db 385 SFVGTAGYVSPEVL 398

Search completed: May 17, 2006, 12:02:22
Job time : 180 secs

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GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 17, 2006, 11:59:34 ; Search time 295 Seconds
(without alignments)
50.170 Million cell updates/sec

Title: US-10-689-576-3
Perfect score: 79
Sequence: 1 ANSFVGTNAVSPPELL 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot 7.2.*
1: uniprot_sprot.*
2: uniprot_crembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	79	100.0	319	Q9UPJ7_HUMAN	Q9UPJ7 homo sapien
2	79	100.0	367	Q9UPJ8_HUMAN	Q9UPJ8 homo sapien
3	79	100.0	396	Q6A1A2_HUMAN	Q6A1A2 homo sapien
4	79	100.0	429	Q9BRD5_HUMAN	Q9BRD5 homo sapien
5	79	100.0	434	Q3UEW8_MOUSE	Q3UEW8 mus musculu
6	79	100.0	492	Q59EH6_HUMAN	Q59EH6 homo sapien
7	79	100.0	522	Q3TRU2_MOUSE	Q3TRU2 mus musculu
8	79	100.0	532	Q8K3I3_MOUSE	Q8K3I3 mus musculu
9	79	100.0	537	Q6NZV1_BRARE	Q6NZV1 brachydactilo
10	79	100.0	551	Q810Z4_MOUSE	Q810Z4 mus musculu
11	79	100.0	556	PDPK1_HUMAN	PDPK1 homo sapien
12	79	100.0	559	Q53HJ5_HUMAN	Q53HJ5 homo sapien
13	79	100.0	556	Q6FI20_HUMAN	Q6FI20 homo sapien
14	79	100.0	556	Q5F3U4_CHICK	Q5F3U4 gallus galli
15	79	100.0	558	Q4S4R0_TESTG	Q4S4R0 tetraodon n
16	79	100.0	559	PDPK1_MOUSE	PDPK1 mus musculu
17	79	100.0	559	1 PDPK1_RAT	Q55173 rattus norv
18	79	100.0	559	Q3UGN6_MOUSE	Q3UGN6 mus musculu
19	79	100.0	559	Q3UHZ0_MOUSE	Q3UHZ0 mus musculu
20	79	100.0	571	Q7BHX2_ASTPE	Q7BHX2 aesterina pe
21	79	92.4	925	Q6CTI4_KULULA	Q6CTI4 kluyveromyc
22	71	89.9	813	Q5B8M0_EMENTI	Q5B8M0 kluyveromyc
23	71	89.9	839	Q4WYD7_ASPPU	Q4WYD7 aspergillus
24	71	89.9	850	Q2UBU7_ASPPU	Q2UBU7 aspergillus
25	71	89.9	1542	Q6CFM7_YARALI	Q6CFM7 yarrowia li
26	70	88.6	686	Q54TW2_DICDI	Q54TW2 dictyosteli
27	70	88.6	726	PKH3_ASHGO	Q733D9 ashybysa gos
28	70	88.6	944	Q5A3P6_CANAL	Q5A3P6 candida alb
29	70	88.6	1062	Q5B1K8_DEBHA	Q5B1K8 debaromyce
30	70	88.6	1153	Q5A3V9_CANAL	Q5A3V9 candida alb
31	69	87.3	822	Q9BHX6_APLCA	Q9BHX6 aplysia cal

32	68	86.1	812	2	Q4HWD3_GIBZE	Q4HWD3 gibberella
33	68	86.1	922	2	Q873K1_NEUCR	Q873K1 neurospora
34	68	86.1	965	2	Q6FT84_CANCA	Q6FT84 candida gla
35	68	86.1	1667	2	Q4P4E1_USITMA	Q4P4E1 usitlago ma
36	67	84.8	484	2	Q7PUX5_ANOGA	Q7PUX5 anophles g
37	67	84.8	647	2	Q6CPN3_KULULA	Q6CPN3 kluyveromyc
38	67	84.8	766	1	PKH1_YEAST	Q03407 saccharomyc
39	67	84.8	991	2	Q6FMN9_CANCA	Q6FMN9 candida gla
40	67	84.8	1033	2	Q753H7_ASHGO	Q753H7 ashybysa gos
41	67	84.8	1076	2	Q6FQ89_CANCA	Q6FQ89 candida gla
42	67	84.8	1081	1	KOKO_YEAST	Q12236 saccharomyc
43	66	83.5	835	1	PDPRK1_DROME	Q9W0V1 drosophila
44	66	83.5	861	2	Q59RK8_CANAL	Q59RK8 candida alb
45	66	83.5	861	2	Q59S09_CANAL	Q59S09 candida alb

ALIGNMENTS

RESULT 1
Q9UPJ7_HUMAN PRELIMINARY; PRT; 319 AA.
ID Q9UPJ7;
AC Q9UPJ7;
DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT 01-MAY-2000, sequence version 1.
DI 21-FEB-2006, entry version 24.
DE 21-FEB-2006, entry version 24.
DN PKB-like (fragment).
GN Name=PKB-like 2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Ricke D.O., Bruce D., Munde M., Doggett N., Munk C., Saunders E.,
RA Robinson D., Jones M., Buckingham J., Chasteen L., Thompson S.,
RA Goodwin L., Bryant J., Tesmer J., Meinke L., Longmire U., White S.,
RA Ueng S., Tatum O., Campbell C., Fawcett J., Maltbie M., Mista M.,
RA Deaven L.,
RN Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
RL [2]
RP NUCLEOTIDE SEQUENCE.
RA Ricke D.O.,
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
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CC
CC EMBL: AC005591; AAC33798.1; -; Genomic_DNA.
DR HSSP; O15530; 1HW.
DR SMR; Q9UPJ7; 1-122.
DR Ensembl: ENSG00000140992; Homo sapiens.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004672; F:protein kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR011993; PH type.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR Pfam; PF00069; Kinase; I.
DR ProDom; PD000001; Prot_kinase; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW ATP-binding; Kinase; Transferase.
FT NON TER 1
SQ SEQUENCE 319 AA; 36620 MW; 01E18FE1B5D4A53 CRC64;
Query Match 100.0%; Score 79; DB 2; Length 319;
Best Local Similarity 100.0%; Pred. No. 4.1e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ANSFVGTNAVSPPELL 16
|||
DB 2 ANSFVGTNAVSPPELL 17

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RESULT 2
Q9UPJ8_HUMAN PRELIMINARY; PRT; 367 AA.
ID Q9UPJ8_HUMAN
AC Q9UPJ8;
DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT 01-MAY-2000, sequence version 1.
DT 07-FEB-2006, entry version 24.
DE PKB-like (Fragment).
GN Name=PKB-like 1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
NCBI_TaxID=9606;
RN Nucleotide Sequence.
RP Rieke D.O., Bruce D., Mundt M., Doggett N., Munk C., Saunders E.,
RA Robinson D., Jones M., Buckingham J., Chasteen L., Thompson S.,
RA Goodwin L., Bryant J., Teemer J., Meincke L., Longmire J., White S.,
RA Ueng S., Tatam O., Campbell C., Fawcett J., Maltbie M., Mista M.,
RA Deaven L.;
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP Nucleotide Sequence.
RA Rieke D.O.;
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
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DR EMBL; AC005591; AAC33797.1; -; Genomic DNA.
DR HSSP; O15530; 1H1W.
DR Ensemble1; ENSG00000140992; Homo sapiens.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0000166; F:nucleotide binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0006468; F:protein amino acid phosphorylation; IEA.
DR GO; GO:0006740; F:transferase activity; IEA.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; Pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR ATP-binding; Kinase; Nucleotide-binding;
KW Serine/threonine-protein kinase; Transferase.
FT NON_TER 1 1
FT NON_TER 367 367
SQ SEQUENCE 367 AA; 41299 MW; 261CDF0075587493 CRC64;

Query Match 100.0%; Score 79; DB 2; Length 367;
Best Local Similarity 100.0%; Pred. No. 4,7e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DT 13-SEP-2004, sequence version 1.
DT 07-FEB-2006, entry version 14.
DE PDPK2 protein.
GN Name=PDPK2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
NCBI_TaxID=9606;
RN Nucleotide Sequence.
RP Tissue=Brain;
RA Pingzhang W., Xin W., Tianjing C., Jun W., Ying L.;
RT "A novel member of human 3-phosphoinositide dependent protein kinase-1
RT family, PDPK2."
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
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DR EMBL; AJ785968; CAH05056.1; -; mRNA.
DR SMR; Q6A1A2; 45-331.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0000166; F:nucleotide binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0006468; F:transferase activity; IEA.
DR GO; GO:0006740; F:transferase activity; IEA.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR ATP-binding; Kinase; Nucleotide-binding;
KW Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 396 AA; 44765 MW; A0661913B473D8DF CRC64;

Query Match 100.0%; Score 79; DB 2; Length 396;
Best Local Similarity 100.0%; Pred. No. 5,1e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3
Q6A1A2_HUMAN PRELIMINARY; PRT; 396 AA.
ID Q6A1A2_HUMAN
AC Q6A1A2;
DT 13-SEP-2004, integrated into UniProtKB/TrEMBL.

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DT 13-SEP-2004, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 14.
DE PDPK2 protein.
GN Name=PDPK2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
NCBI_TaxID=9606;
RN Nucleotide Sequence.
RP Tissue=Brain, and uterus;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,

```

RA Datchenko L., Marsina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stepien M., Soares M.B., Bonaldi M.F., Casavert T.L., Scheetz T.E.,
RA Brownstein W.J., Usdin T.B., Toshynki S., Carrinct P., Prange C.,
Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
Ra Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Villalon D.K., Muzy D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Helton E., Ketteman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002) .

RN [2]
RN NCLEOTIDE SEQUENCE.
RP TISSUE=Brain;
RC NIH MG Project;
RD Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.

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CC -----

DR EMBL; BC006339; AAH06339.2; -; mRNA.
DR EMBL; BC033494; AAA33494.1; -; mRNA.
DR HSSP; I05530; IHM.
DR SMK; Q9BRD5; 101-231, 282-429.
DR Ensembl; ENSG00000140992; Homo sapiens.
DR Linkhub; Q9BRD5; -;
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0000166; F:nucleotide binding; IEA.
DR DR GO; GO:0004672; F:protein kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006466; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPRO11933; PH type.
DR InterPro; IPRO0719; Prot_Kinase.
DR InterPro; IPRO02290; Ser_thr_kinase.
DR Pfam; PF00069; Kinase_2.
DR ProDom; PD000001; Prot_kinase; 1.
DR PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.
DR ATP-binding; Kinase; Nucleotide-Binding; Transferase.
KW AMYLOIDosis; Amyloid; Alzheimer's Disease; Senile plaques;
SQ SEQUENCE 429 AA; 48201 MW; 860C8A8C0616ICE1 CRC64;

DQ Query Match 100.0%; Score 79; DB 2; Length 429;
Best Local Similarity 100.0%; Pred. No. 5.5e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0

Db 1 ANSPVGTAGTVSPELL 16
||| ||||||||
112 ANSFVGTAQTYSPELL 127

RESULT 5
Q3UENB_MOUSE PRELIMINARY; PRT; 434 AA.
AC Q3UENB_MOUSE
DT 11-OCT-2005, integrated into UniProtKB/TREMBL.
DT 11-OCT-2005, sequence version 1.
DE 07-FEB-2006, entry version 6.
DE Adult retina cDNA, RIKEN full-length enriched library,
clone:A930012K24 product:j-3-phosphoinositide dependent protein kinase-
1, full insert sequence. (Fragment).
GN Name=Pdk1;
OS Mus musculus (Mouse);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muroidea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Retina;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning."
RL Methods Enzymol. 303:19-44(1999).
RN [2]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Retina;
RX PubMed=16141072; DOI=10.1126/science.1112014;
RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
RA Oyama R., Ravasi T., Lenhard B., Wells C., Kodius R., Shimokawa K.,
RA Bajic V.B., Bremner S.E., Batalov S., Forrest A.R., Zavolan M.,
RA Davis M.J., Wilmring L.G., Altshul V., Allen J.E.,
RA Ambesi-Improbato A., Avelar R., Accuratiya R.N., Bailey T.L.,
RA Banasi M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
RA Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
RA Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
RA di Bernardo D., Down T., Engstrom P., Fagiolini M., Faulner G.,
RA Fletcher C.F., Fukushima T., Furuno M., Furki S., Gariboldi M.,
RA Georgi-Hemming P., Gingeras T., Purno M., Putek S., Gariboldi M.,
RA Guertlich S., Harbers M., Hayashi Y., Henrich T.K., Hirokawa N.,
RA Hill D., Huhniacki L., Iacono M., Ieko K., Iwama A., Isikawa T.,
RA Jait M., Knapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
RA Kitano H., Kollas G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
RA Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
RA Lunni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
RA Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
RA Motusaki-Tahar S., Mulder N., Nakano N., Nakauchi H., Ng P.,
RA Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
RA Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavese G., Pesole G.,
RA Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
RA Roost B., Ruan Y., Salzberg S.L., Sandlin A., Schneider C.,
RA Schonbach C., Sekiguchi K., Semple C.A., Sero S., Sessa L., Sheng Y.,
RA Shibata Y., Shimada E., Shimada K., Silva D., Sinclair B.,
RA Sperling S., Stupka E., Sugura K., Sultana R., Takenaka Y., Taki K.,
RA Tammoja K., Tan S.L., Tang S., Taylor S., Tegner J., Teichmann S.A.,
RA Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yeig K.,
RA Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide M., Bult C.,
RA Gilmour S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
RA Walstedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
RA Furuta S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
RA Iida Y., Iemura K., Itoh M., Kato T., Kawaji H., Kawagashita N.,
RA Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Nimomiya N.,
RA Nishio T., Okada M., Plessey C., Shibata K., Shiraki T., Suzuki S.,
RA Tegami M., Waki K., Wataniki A., Okamura-Ohno Y., Suzuki H., Kawai J.,
RA Hayashizaki Y.;
RT "The transcriptional landscape of the mammalian genome."
RL Science 309:1559-1563(2005).
RN [3]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Retina;
RX PubMed=16141073; DOI=10.1126/science.1112009;
RA RIKEN Genome Exploration Research Group, and Genome Science Group
RG (Genome Network Core Team) and the FANTOM Consortium;
RT "Antisense transcription in the Mammalian Transcriptome."
RL Science 309:1564-1566(2005).
RN [4]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Retina;
RX MEDLINE=22354683; PubMed=12466551; DOI=10.1038/nature01265;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi U., Bono H., Kondo S.,
RA Nishio T., Oshio N., Saito R., Suzuki H., Yamana K., Kiyosawa H.,
RA Yeig K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C.,
RA Baldairelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schirral L.M., Knapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chochla C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Gorkik A., Gough J.,
RA Gilmour S., Guertlich S., Hirokawa N., Jackson I.J., Jarvis E.D.,

RA Kanai A., Kawai H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Kanagaya A., Kurochkin I.V., Lee Y., Lehnard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagasima T., Numa K., Okido T., Pavan W.J., Pette G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.V., Qi D., Ramchandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sanderlin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takemura Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Vercaro R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilm L.G., Wyszewski B., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer P., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Alzawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shigenaga A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.,
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573(2002).
[5]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=C57BL/6J; TISSUE=Retina;
RC MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RX Kawai J., Shigenaga A., Shibata K., Yoshino M., Itoh M.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K.I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochava H.,
RA Knehl L.M., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schiraldi L.M., Straubli F., Suzuki R., Tomita M., Wagner L., Watanabe Y.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barin G.,
RA Blake J., Botfield D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Hume D.A., Kamita M.,
RA Guncionich S., Hill D., Hofmann M., Hume D.A., Kamita M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombere P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seye T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilm L.,
RA Wyszewski B., Yoshida K., Hasegawa Y., Kawai H., Konteuk S.,
RA Hayashizaki Y.,
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690(2001).
[6]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=C57BL/6J; TISSUE=Retina;
RC MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600.
RX Shibata K., Itoh M., Alzawa K., Nagao K., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitamura T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Makunoto H., Sakaguchi S., Ikegami T., Kasahagi K.,
RA Fujisawa S., Inoue K., Togawa Y., Izawa M., Ohara E., Matsubara M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsubara S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kita A., Hayashizaki Y.,
RT "IKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multiplexed capillary sequencer."
RL Genome Res. 10:1757-1771(2000).
[8]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=C57BL/6J; TISSUE=Retina;
RC Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,
RA Hori F., Iida J., Imanura K., Imotani K., Itoh M., Kanagawa S.,
RA Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N.,

RA Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D.,
RA Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watanabe A.,
RA Muramatsu M., Hayashizaki Y.,
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
CC -1-SIMILARITY: Belongs to the Ser/Thr protein kinase family.
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NonDerivative License
CC EMBL; AK149289; BAE28793.1; -- mRNA.
DR MG1; MG1:1338068; Pdpk1.
DR GO; GO:0005737; C:cytoplasm; IDA.
DR GO; GO:0016023; C:cytoplasmic membrane-bound vesicle; IDA.
DR GO; GO:0004676; F:3-phosphoinositide-dependent protein kinase. . . ; IDA.
DR GO; GO:0006972; P:hyperosmotic response; IDA.
DR GO; GO:0007165; P:signal transduction; TAS.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_Thr_kinase.
DR InterPro; IPR002290; Ser_Thr_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Nucleotide-binding;
KW Serine/threonine-protein kinase; Transferase.
FT NON_TER 434
SQ SEQUENCE 434 AA; 48960 MW; 161630FB56FC793F CRC64;
Query Match 100.0%; Score 79; DB 2; Length 434;
Best Local Similarity 100.0%; Pred. No. 5.6e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ANSFVGTQAYVSPDL 16
DB 242 ANSFVGTQAYVSPDL 257
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ID 059EH6 HUMAN PRELIMINARY; PRT; 492 AA.
AC 059EH6;
DT 26-APR-2005, integrated into UniProtKB/TrEMBL.
DT 26-APR-2005, sequence version 1.
DT 07-FEB-2006, entry version 7.
DE 3-phosphoinositide dependent protein kinase-1 variant (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eumetazoa;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RA Totoki Y., Toyoda A., Takeda T., Sakaki Y., Tanaka A., Yokoyama S.,
RA Ohara O., Nagase T., Kikuno F.R.;
RT "None Title."
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
CC -1-SIMILARITY: Belongs to the Ser/Thr protein kinase family.
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NonDerivative License
CC EMBL; AB209835; BAD93072.1; -- mRNA.
DR SMR; 059EH6; 110-396.
DR Ensembl; ENSG00000140992; Homo sapiens.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0000166; F:nucleotide binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.

DR InterPro: IPR000169; Pept_Cys_AS.
 DR InterPro: IPR000719; Prot_Kinase.
 DR InterPro: IPR008271; Ser_thr_Pkin_AS.
 DR InterPro: IPR002290; Ser_thr_Pkinase.
 DR InterPro: IPR001245; Tyr_Pkinase.
 DR Pfam: PF00069; Pkinase; 1.
 DR SMART: SM00220; S_TKC; 1.
 DR PROSITE: PS00107; PROTEIN KINASE ATP; UNKNOWN_1.
 DR PROSITE: PS50011; PROTEIN KINASE DOM; 1.
 DR PROSITE: PS00108; PROTEIN KINASE ST; 1.
 DR PROSITE: PS00139; THIOL PROTEASE CYS; UNKNOWN_1.
 KW ATP-binding; Kinase; Nucleotide-binding.
 KW Serine/threonine-protein kinase; Transferase.
 FT NON TER 1
 SQ SEQUENCE 492 AA; 54828 MW; ABBA2A6F7C986E26 CRC64;
 Query Match 100.0%; Score 79; DB 2; Length 492;
 Best Local Similarity 100.0%; Pred. No. 6,4e-05;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ANSPVGTQVYSPILL 16
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 Db 277 ANSPVGTQVYSPILL 292

RESULT 7
 ID Q3TRL2 MOUSE PRELIMINARY; PRT; 522 AA.
 AC Q3TRL2;
 DT 11-OCT-2005, integrated into UniProtKB/TrEMBL.
 DT 11-OCT-2005, sequence version 1.
 DT 07-FEB-2006, entry version 7.
 DE Adult female vagina cDNA, RIKEN full-length enriched library,
 DE clone:930010W10 product:3-phosphoinositide dependent protein kinase-
 DE 1, full insert sequence.
 GN Name=Pdk1;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Vagina;
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning."
 RL Methods Enzymol. 303:19-44(1999).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Vagina;
 RX PubMed=16141072; DOI=10.1126/science.1112014;
 RA Carninci P., Kasukawa T., Katayama S., Gough J., Fritch M.C., Maeda N.,
 RA Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
 RA Bajic V.B., Bremner S.E., Batalov S., Forrest A.R., Zavolan M.,
 RA Davis M.U., Wilming L.G., Aldridge V., Allen J.E.,
 RA Amemiya-Impombato A., Apweiler R., Acurialiya R.N., Bailey T.L.,
 RA Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
 RA Chiu K.P., Choudhary V., Christoffels A., Clutierbuch D.R.,
 RA Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
 RA di Bernardo D., Down T., Engstrom P., Fagioli M., Faulkner G.,
 RA Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gabold M.,
 RA Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
 RA Guentrich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
 RA Hill D., Hummel L., Iacono M., Ikeo K., Iwama A., Ishikawa H.,
 RA Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
 RA Kitano H., Kollias G., Kriehnan S.P., Kruger A., Kummerfeld S.K.,
 RA Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
 RA Liu J., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
 RA Matsumura H., Matsuzawa S., Miki N., Mignone F., Miyake S., Morris K.,
 RA Mortazavi-Arab S., Mulder N., Nakano N., Nakamura H., Ng P.,
 RA Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
 RA Okazaki Y., Orlano V., Pang K.C., Pavan W.J., Pavani G., Pesole G.,

RA Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
 RA Roel B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
 RA Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,
 RA Shibusaki Y., Shimada H., Shimada K., Silva D., Sindelar B.,
 RA Sperling S., Stupka E., Sugiyama K., Sultana R., Takenaka Y., Taki K.,
 RA Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
 RA Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yang K.,
 RA Yamashita H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bull C.,
 RA Yamanishi S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
 RA Wahlestedt C., Waltick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
 RA Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki T., Arakawa T.,
 RA Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
 RA Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Niimura N.,
 RA Nishio T., Okada M., Pleasy C., Shibata K., Shiraki T., Suzuki S.,
 RA Tagami M., Waki K., Watanabe A., Okamura-Oho Y., Suzuki H., Kawai J.,
 RA Hayashizaki Y.;
 RT "The transcriptional landscape of the mammalian genome."
 RL Science 309:1559-1563(2005).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Vagina;
 RX PubMed=16141073; DOI=10.1126/science.1112009;
 RG RIKEN Genome Exploration Research Group, and Genome Science Group
 RG (Genome Network Core Team) and the FANTOM Consortium;
 RT "Antisense Transcription in the Mammalian Transcriptome";
 RL Science 309:1564-1566(2005).
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Vagina;
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nikaido I., Oeato N., Saito R., Suzuki H., Yamataka I., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Haegawa Y., Nogami A., Schonbach C., Gojobori T.,
 RA Baldarelli R., Hill D.P., Bull C., Hume D.A., Quackenbush J.,
 RA Schirrali L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
 RA Blake J.A., Brad D., Bruscia V., Chochia C., Corbani L.B., Cousins S.,
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
 RA Grimmond S., Guentrich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kanai A., Kawai H., Kawasawa Y., Kedzierski R.M., King P.A.,
 RA Kongsawa A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Nemata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
 RA Ravasi T., Reed J.C., Reid J., Ring B.Z., Ringwald M.,
 RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
 RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wilming L.G., Wyszynski-Boris A., Yangisawa M., Yang I., Yang L.,
 RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 RA Hitozane-Kishikawa T., Konno H., Nakamura M., Sakazune N., Sato K.,
 RA Shiraki T., Waki K., Kawai K., Aizawa K., Arakawa T., Fukuda S.,
 RA Hara A., Hashizume W., Imocani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs."
 RL Nature 420:563-573(2002).
 RN [5]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Vagina;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Iwama M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fletschmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schirrali L.M., Stubbli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barish G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

RA Brownstein M.J., Bulic C., Fletcher C., Fujita M., Gariboldi M.,
 RA Guetlich S., Hill D., Hofmann M., Hume D.A., Kamitaya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombere P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoendach C., Seiya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyo-Oka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Wyshaw-Borle A., Yoshida K., Hasegawa Y., Kawaji H., Kohlschki S.,
 RA Hayaishizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection";
 RL Nature 409:685-690(2001).
 RN [6]
 RP NUCLEOTIDE SEQUENCE.
 RC STAIN=C57BL/6J; TISSUE=Vagina;
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.,
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes";
 RL Genome Res. 10:1617-1630(2000).
 RN [7]
 RP NUCLEOTIDE SEQUENCE.
 RC STAIN=C57BL/6J; TISSUE=Vagina;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Azawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Kono H., Akiyama J., Nishi K., Kitsuana T., Tashiro H., Itoh M.,
 RA Suni N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kasahagi K.,
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer";
 RL Genome Res. 10:1757-1771(2000).
 RN [8]
 RP NUCLEOTIDE SEQUENCE.
 RC STAIN=C57BL/6J; TISSUE=Vagina;
 RA Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,
 RA Hoti F., Iida J., Imanura K., Imotani K., Itoh M., Kanagawa S.,
 RA Kawai J., Kojima M., Kono H., Murata M., Nakamura M., Ninomiya N.,
 RA Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D.,
 RA Shibata K., Shitaki T., Tagami M., Tagami Y., Waki K., Wataniki A.,
 RA Muramatsu M., Hayaishizaki Y.;
 RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- SMILARITY: Belongs to the Ser/Thr protein kinase family.
 CC -----
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 CC -----
 DR EMBL: AK162677; BA037017.1; -; mRNA.
 DR MGI: MGI:1338068; Pdk1.
 DR GO: GO:0005737; C:cytoplasmic membrane-bound vesicle; IDA.
 DR GO: GO:0016023; C:cytoplasmic membrane-bound vesicle; IDA.
 DR GO: GO:0004676; F:3-phosphoinositide-dependent protein kinase. .; IDA.
 DR GO: GO:0006972; P:hyperosmotic response; IDA.
 DR GO: GO:0007165; P:signal transduction; TAS.
 DR InterPro: IPR000719; Prot. kinase.
 DR InterPro: IPR008271; Ser_thr_pkin_AS.
 DR InterPro: IPR002290; Ser_thr_pkinase.
 DR InterPro: IPR001245; Tyr_pkinase.
 DR Pfam: PF00069; Pkinase; 1.
 DR ProDom: PD000001; Prot. kinase; 1.
 DR SMART: SM00220; S_TKc; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 DR ATP-binding; Kinase; Nucleotide-binding;
 KM Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 522 AA; 59328 MW; 4C31B7D53F6306BF CRC64;

Query Match 100.0%; Score 79; DB 2; Length 522;
 Best Local Similarity 100.0%; Pred. No. 6; 9e-05;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ANSFVGTAGVYSPPELL 16
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 Db 242 ANSFVGTAGVYSPPELL 257
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 RESULT 8
 ID 08KJL3 MOUSE PRELIMINARY; PRT; 532 AA.
 AC 08KJL3;
 DT 01-OCT-2002, integrated into UniProtKB/TrEMBL.
 DT 01-OCT-2002, sequence version 1.
 DT 21-FEB-2006, entry version 22.
 DE Phosphoinositide-dependent protein kinase-1 beta.
 GN Name=Pdk1; Synonyms=Pdk1beta;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22050196; PubMed=12054753; DOI=10.1016/S0006-291X(02)00449-7;
 RA Dong L.Q., Ramos F.J., Wick M.J., Lim M.A., Guo Z., Strong R.,
 RA Richardson A., Liu F.;
 RT "Cloning and characterization of a testis and brain-specific isoform
 RT of mouse 3'-phosphoinositide-dependent protein kinase-1, mPDK-1
 RT beta";
 RL Blochm. Biophys. Res. Commun. 294:136-144(2002).
 CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 CC -1- SMILARITY: Belongs to the Ser/Thr protein kinase family.
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 CC -----
 DR EMBL: AY062008; AL47185.1; -; mRNA.
 DR HSSP: O15530; 1H1W.
 DR SMR: 08KJL3; 48-334, 385-532.
 DR Ensemble: ENSMUSG00000024122; Mus musculus.
 DR MGI: MGI:1338068; Pdk1.
 DR GO: GO:0005737; C:cytoplasm; IDA.
 DR GO: GO:0016023; C:cytoplasmic membrane-bound vesicle; IDA.
 DR GO: GO:0004676; F:3-phosphoinositide-dependent protein kinase. .; IDA.
 DR GO: GO:0006972; P:hyperosmotic response; IDA.
 DR GO: GO:0007165; P:signal transduction; TAS.
 DR InterPro: IPR011993; PH type.
 DR InterPro: IPR000719; Prot. kinase.
 DR InterPro: IPR008271; Ser_thr_pkin_AS.
 DR InterPro: IPR002290; Ser_thr_pkinase.
 DR InterPro: IPR001245; Tyr_pkinase.
 DR Pfam: PF00069; Pkinase; 1.
 DR ProDom: PD000001; Prot. kinase; 1.
 DR SMART: SM00220; S_TKc; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 DR ATP-binding; Kinase; Nucleotide-binding;
 KM Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 532 AA; 60934 MW; F90731C7ECDBE569 CRC64;

Query Match 100.0%; Score 79; DB 2; Length 532;
 Best Local Similarity 100.0%; Pred. No. 6; 9e-05;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ANSFVGTAGVYSPPELL 16
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 Db 215 ANSFVGTAGVYSPPELL 230
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RESULT 9
 ID 06NZVL BRARE PRELIMINARY; PRT; 537 AA.
 AC 06NZVL;
 DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.

DT 05-JUN-2004, sequence version 1.
 DT 21-FEB-2006, entry version 20.
 DE Hypothetical protein zgc:77318.
 GN ORFNames=zgc:77318;
 OS Brachydanio rerio (zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 CC NCBI_TaxID=7955;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Embryo;
 RX MEDLINE=22388257, PubMed=12477932, DOI=10.1073/pnas.242603899;
 RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buelow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Ditchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carrinci P., Prange C.,
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Embryo;
 RG NIH MGC Project;
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NonDerivs license
 CC -----
 CC EMBL; BC065959; AAH65959.1; -; mRNA.
 DR HSSP; Q63450; 1A06.
 DR SMR; Q6N2V1; 51-336, 397-532.
 DR Ensembl; ENSDARG0000018285; Danio rerio.
 DR ZFIN; ZDB-GENE-040426-1820; zgc:77318.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0000166; F:nucleotide binding; IEA.
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR InterPro; IPR011993; Pk_type.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR008271; Ser_thr_pkin_AS.
 DR InterPro; IPR002290; Ser_thr_pkinase.
 DR InterPro; IPR01245; Tyr_pkinase.
 DR Pfam; PF00069; Pkinase; 1.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00220; S_TKc; 1.
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE; PS0011; PROTEIN KINASE DOM; 1.
 DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
 KW ATP-binding; Hypothetical protein; Kinase; Nucleotide-binding;
 KW Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 537 AA; 61450 MW; 20A0FED4E0A79D6F CRC64;

Query Match 100.0%; Score 79; DB 2; Length 537;
 Best Local Similarity 100.0%; Pred. No. 7e-05;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ANSFVGTAGVSPRL 16
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 Db 217 ANSFVGTAGVSPRL 232
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 ID Q81024_MOUSE PRELIMINARY; PRT; 551 AA.
 AC Q81024_MOUSE
 DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.
 DT 01-JUN-2003, sequence version 1.
 DT 07-FEB-2006, entry version 15.
 DE PDK1 (Fragment).
 DE Name=pdk1;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 CC NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=129/SVJ;
 RA Brachwaite M., Waelz P., Schlessinger D., Nagaraja R.;
 RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NonDerivs license
 CC -----
 CC EMBL; AY162410; AA017164.1; -; Genomic DNA.
 DR HSSP; O15530; 1H1W.
 DR SMR; Q81024; 67-353, 404-551.
 DR Ensembl; ENSMUSG0000024122; Mus musculus.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0000166; F:nucleotide binding; IEA.
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR InterPro; IPR011993; Pk_type.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR008271; Ser_thr_pkin_AS.
 DR InterPro; IPR002290; Ser_thr_pkinase.
 DR InterPro; IPR01245; Tyr_pkinase.
 DR Pfam; PF00069; Pkinase; 1.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00220; S_TKc; 1.
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE; PS0011; PROTEIN KINASE DOM; 1.
 DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
 KW ATP-binding; Kinase; Nucleotide-binding;
 KW Serine/threonine-protein kinase; Transferase.
 FT NON TER 1
 SQ SEQUENCE 551 AA; 62870 MW; ACC31D51439282F4 CRC64;

Query Match 100.0%; Score 79; DB 2; Length 551;
 Best Local Similarity 100.0%; Pred. No. 7.2e-05;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ANSFVGTAGVSPRL 16
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 Db 234 ANSFVGTAGVSPRL 249
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 ID PDK1_HUMAN STANDARD; PRT; 556 AA.
 AC O15530;
 DT 18-OCT-2001, integrated into UniProtKB/Swiss-Prot.
 DT 01-JAN-1998, sequence version 1.
 DT 07-MAR-2006, entry version 58.
 DE 3-phosphoinositide-dependent protein kinase 1 (EC 2.7.1.37) (hPDK1).
 GN Name=PDK1; Synonyms=PDK1;
 OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
 OC Homo.
 OC NCBI Taxid=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [mRNA] (ISOFORM 1).
 RX MEDLINE=97250749; PubMed=9094314; DOI=10.1016/S0960-9822(06)00122-9;
 RA Alessi D.R., James S.R., Downes C.P., Holmes A.B., Gaffney P.R.J.,
 RA Reese C.B., Cohen P.;
 RT "Characterization of a 3-phosphoinositide-dependent protein kinase
 RT which phosphorylates and activates protein kinase B alpha";
 RL Curr. Biol. 7:261-269(1997).
 RN [2]
 RP NUCLEOTIDE SEQUENCE [mRNA] (ISOFORM 1).
 RX MEDLINE=98035195; PubMed=9368760; DOI=10.1016/S0960-9822(06)00336-8;
 RA Alessi D.R., Deak M., Casamayor A., Caudwell F.B., Morrice N.A.,
 RA Norman D.G., Gaffney P.R.J., Reese C.B., MacDougall C.N., Harbison D.,
 RA Ashworth A., Bowles M.;
 RT "3-phosphoinositide-dependent protein kinase-1 (PDK1): structural and
 RT functional homology with the Drosophila DSTRPK1 kinase.";
 RL Curr. Biol. 7:776-789(1997).
 RN [3]
 RP NUCLEOTIDE SEQUENCE [mRNA] (ISOFORMS 1 AND 3).
 RC TISSUE=Myeloid;
 RX MEDLINE=98111410; PubMed=9445477; DOI=10.1126/science.279.5351.710;
 RA Stephens L.R., Anderson K.E., Stokoe D., Erdjument-Bromage H.,
 RA Painter G.F., Holmes A.B., Gaffney P.R.J., Reese C.B., McCormick F.,
 RA Tempst P., Coadwell W.J., Hawkins P.T.;
 RT "Protein kinase B kinases that mediate phosphatidylinositol 3,4,5-
 RT trisphosphate-dependent activation of protein kinase B";
 RL Science 279:710-714(1998).
 RN [4]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
 RC TISSUE=Kidney;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strauberg R.L., Feinold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
 RA Datchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stepien M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carrinci P., Prange C.,
 RA Bata S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mulhally S.J.,
 RA Raskas S.A., McMan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Vallatton D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Faney J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [5]
 RP MUTAGENESIS OF ARG-474, AND ALTERNATIVE SPLICING.
 RX MEDLINE=98301766; PubMed=9637919; DOI=10.1016/S0960-9822(98)70274-X;
 RA Anderson K.E., Coadwell W.J., Stephens L.R., Hawkins P.T.;
 RT "Translocation of PDK-1 to the plasma membrane is important in
 RT allowing PDK-1 to activate protein kinase B";
 RL Curr. Biol. 8:684-691(1998).
 RN [6]
 RP PHOSPHORYLATION SITES SER-25, SER-241, SER-393, SER-396 AND SER-410,
 RP AND MUTAGENESIS OF TYR-9, TYR-373 AND TYR-376, AND
 RX MEDLINE=99386657; PubMed=10455013; DOI=10.1042/0264-6021.3420287;
 RA Casamayor A., Morrice N.A., Alessi D.R.;
 RT "Phosphorylation of Ser-241 is essential for the activity of 3-
 RT phosphoinositide-dependent protein kinase-1: identification of five
 RT sites of phosphorylation in vivo";
 RL Biochem. J. 342:287-292(1999).
 RN [7]
 RP MUTAGENESIS OF ALA-277.
 RX MEDLINE=99292684; PubMed=10364160;
 RA Paradis S., Allion M., Toker A., Thomas J.H., Ruvkun G.;
 RT "A PDK1 homolog is necessary and sufficient to transduce AGE-1 PI3
 RT kinase signals that regulate diapause in *Caenorhabditis elegans*";
 RL Genes Dev. 13:1438-1452(1999).
 RN [8]
 RP PHOSPHORYLATION SITES TYR-9, SER-241, TYR-373 AND TYR-376, AND
 RP MUTAGENESIS OF TYR-9, TYR-373 AND TYR-376.
 RX MEDLINE=21463095; PubMed=11481331; DOI=10.1074/jbc.M105916200;
 RA Park J., Hill M.M., Hees D., Brazill D.P., Hofsteenge J.,
 RA Hemmings B.A.;
 RT "Identification of tyrosine phosphorylation sites on 3-
 RT phosphoinositide-dependent protein kinase-1 (PDK1) and their role in
 RT regulating kinase activity";
 RL J. Biol. Chem. 276:37459-37471(2001).
 RN [9]
 RP PHOSPHORYLATION SITE SER-241.
 RX PubMed=15302935; DOI=10.1073/pnas.0404720101;
 RA Beaulieu S.A., Jedrychowski M., Schwartz D., Elias J.E., Villen J.,
 RA Li J., Cohn M.A., Cantley L.C., Gygi S.P.;
 RT "Large-scale characterization of HeLa cell nuclear phosphoproteins";
 RL Proc. Natl. Acad. Sci. U.S.A. 101:12130-12135(2004).
 CC -1- FUNCTION: Phosphorylates and activates not only PKB/AKT, but also
 CC PKA, PKC-zeta, p70S6K and p90S6K/RSK. May play a general role in
 CC signaling processes and in development (By similarity). Isoform 3
 CC is catalytically inactive.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic and membrane-associated after
 CC cell stimulation leading to its translocation. Tyrosine
 CC phosphorylation seems to occur only at the plasma membrane.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Name=1;
 CC isoId=015530-1; Sequence=Displayed;
 CC Name=2;
 CC isoId=015530-2; Sequence=VSP_004894;
 CC Name=3;
 CC isoId=015530-3; Sequence=VSP_004895;
 CC -1- TISSUE SPECIFICITY: Appears to be expressed ubiquitously.
 CC -1- PTM: Phosphorylated on tyrosine and serine/threonine.
 CC Phosphorylation on Ser-241 in the activation loop is required for
 CC full activity. PDK1 itself can autophosphorylate Ser-241, leading
 CC to its own activation.
 CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PDK1
 CC subfamily.
 CC -1- SIMILARITY: Contains 1 PH domain.
 CC -----
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 CC -----
 DR EMBL, AF017995; AAC51825.1; -, mRNA.
 DR EMBL, Y15056; CA475341.1; -, mRNA.
 DR EMBL, BC012103; AA012103.1; -, mRNA.
 DR PDB, 1H1W; X-ray; A=71-359.
 DR PDB, 1OKY; X-ray; A=51-360.
 DR PDB, 1UTJ; X-ray; A=51-360.
 DR PDB, 1UTU; X-ray; A=51-360.
 DR PDB, 1UUG; X-ray; A=51-360.
 DR PDB, 1UUG; X-ray; A=72-357.
 DR PDB, 1UV9; X-ray; A=71-359.
 DR PDB, 1W1G; X-ray; A=409-556.
 DR PDB, 1W1G; X-ray; A=409-556.
 DR PDB, 1W1H; X-ray; A/B/C/D=409-556.
 DR PDB, 1Z5W; X-ray; A=74-359.
 DR PDB, 2B1Y; X-ray; A=51-360.
 DR Ensemble1; ENSG00000140392; Homo sapiens.
 DR H-invDB; HIX0012732; -;
 DR HGNC; HGNC:8816; PDK1.
 DR MIM; 605213; gene.
 DR LinkHub; O15530; -;
 DR GO; GO:0005737; Cytoplasm; IEP.
 DR GO; GO:0005886; Cytoplasmic membrane; IEP.

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DR GO:0004676; F:3-phosphoinositide-dependent protein kinase. . .; TAS.
DR GO:0030036; P:actin cytoskeleton organization and biogenesis; TAS.
DR GO:0008286; P:insulin receptor signaling pathway; TAS.
DR GO:0006468; P:protein amino acid phosphorylation; TAS.
DR InterPro: IPR01849; PH.
DR InterPro: IPR01993; PH type.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR008271; Ser_thr_pkin_AS.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR InterPro: IPR001245; Tyr_pkinase.
DR Pfam: PF00069; Pkinase; 1.
DR ProDom: PD000001; Prot_kinase; 1.
DR SMART: SM00220; S_TKc; 1.
DR PROSITE: PS50003; PH DOMAIN; FALSE_NEG.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
DR 3D-structure: Alternative splicing; ATP-binding; Kinase; Membrane;
KW Nucleotide-binding; Phosphorylation; Serine/threonine-protein kinase;
KW Transferase.
FT CHAIN 1 556
FT 3-phosphoinositide-dependent protein
FT kinase 1.
FT /FTid=PRO_0000086500.
FT DOMAIN 82 342
FT NP_BIND 459 550
FT COMPBIAS 88 96
FT ACT_SITE 389 398
FT BINDING 205 205
FT BINDING 111 111
FT MOD_RSS 9 9
FT MOD_RSS 25 25
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FT MOD_RSS 373 373
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FT MOD_RSS 410 410
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FT VASPLIC 238 263
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FT MUTAGEN 25 25
FT MUTAGEN 241 241
FT MUTAGEN 277 277
Query Match 100.0%; Score 79; DB 1; Length 556;
Best Local Similarity 100.0%; Pred. No. 7.2e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 ANSFVGTAGVSPPELL 16
DB 239 ANSFVGTAGVSPPELL 254

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RA Maruyama K., Sugano S.;
RT "Oligo-capping: a simple method to replace the cap structure of
RT eucaryotic mRNAs with oligoribonucleotides.";
RL Gene 138:171-174 (1994).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Coronary artery;
RX MEDLINE=96038986; Pubmed=9373149; DOI=10.1016/S0378-1119(97)00411-3;
RA Suzuki Y., Yoshitomo K., Maruyama K., Sugano S.;
RT "Construction and characterization of a full length-enriched and a 5'-
RT end-enriched cDNA library.";
RL Gene 200:149-156 (1997).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Coronary artery;
RA Suzuki Y., Sugano S., Totoki Y., Toyoda A., Takeda T., Sakaki Y.,
RA Tanaka A., Yokoyama S.;
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
CC -I- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
CC -----
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CC Distributed under the Creative Commons Attribution-NonDerivative License
CC -----
DR EMBL: AK222581; BAD96301.1; -; mRNA.
DR SMR: O53HJ9; 72-358, 409-556.
DR Ensembl: ENSG00000140992; Homo sapiens.
DR GO:0005524; F:ATP binding; IEA.
DR GO:0000166; F:nucleotide binding; IEA.
DR GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO:0016740; F:transferase activity; IEA.
DR GO:000468; P:protein amino acid phosphorylation; IEA.
DR InterPro: IPR01993; PH type.
DR InterPro: IPR00719; Prot_kinase.
DR InterPro: IPR008271; Ser_thr_pkin_AS.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR InterPro: IPR001245; Tyr_pkinase.
DR Pfam: PF00069; Pkinase; 1.
DR ProDom: PD000001; Prot_kinase; 1.
DR SMART: SM00220; S_TKc; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Nucleotide-binding;
KW Serine/threonine-protein kinase; Transferase.
FT NON_TER 1
FT SEQUENCE 556 AA; 63126 MW; BBE04F6B7C7D958C CRC64;
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Query Match 100.0%; Score 79; DB 2; Length 556;
Best Local Similarity 100.0%; Pred. No. 7.2e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 ANSFVGTAGVSPPELL 16
DB 239 ANSFVGTAGVSPPELL 254

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RA Neubert P., Keirang K., Schatten R., Shen B., Henze S., Mar W.,
RA Korn B., Zuo D., Hu Y., Labaer J.,
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
CC -----
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CC -----
DR EMBL; CR356517; CAG38755.1; -; mRNA.
DR SMR; Q6F120; 72-358; 409-556.
DR Ensembl; ENSG00000140992; Homo sapiens.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0000166; F:nucleotide binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR011993; PH type.
DR InterPro; IPR008271; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kin_AS.
DR InterPro; IPR01245; Tyr_kinase.
DR Pfam; PF00069; Pkinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; UNKNOWN_1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR ATP-binding; Kinase; Nucleotide-binding;
KM Serine/threonine-protein kinase; transferase.
SQ SEQUENCE 556 AA; 63152 MW; ED8C0306DC4D0653 CRC64;

Query Match 100.0%; Score 79; DB 2; Length 556;
Best Local Similarity 100.0%; Pred. No. 7.2e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ANSFVGTAYVSPPELL 16
Db 239 ANSFVGTAYVSPPELL 254

RESULT 14
Q5F3U4 CHICK PRELIMINARY; PRT; 556 AA.
AC Q5F3U4
DT 15-MAR-2005, integrated into UniProtKB/TrEMBL.
DT 15-MAR-2005, sequence version 1.
DT 21-FEB-2006, entry version 10.
DE Hypothetical protein.
GN ORFNames=RCJMB04.6p10;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OC NCBI_TaxId=9031;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CB; TISSUE=Bursa;
RA Caldwell R.B., Kierzek A.M., Arakawa H., Bezzubov Y., Zaim J.,
RA Fedler P., Kuter S., Blagodatki A., Kostovska D., Koter M.,
RA Plachy J., Carninci P., Hayashizaki Y., Buerstedde J.M.;
RT "Full-length cDNAs from chicken bursa lymphocytes to facilitate
RT gene function analysis.";
RL Genome Biol. 6:R6-R6(2005).
CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AJ851556; CAH65190.1; -; mRNA.
DR SMR; Q5F3U4; 75-361; 412-555.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0000166; F:nucleotide binding; IEA.

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DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR011993; PH type.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_kin_AS.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR01245; Tyr_kinase.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; UNKNOWN_1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR ATP-binding; Hypothetical protein; Kinase; Nucleotide-binding;
KM Serine/threonine-protein kinase; transferase.
SQ SEQUENCE 556 AA; 63068 MW; E1E935D6C3E04C9 CRC64;

Query Match 100.0%; Score 79; DB 2; Length 556;
Best Local Similarity 100.0%; Pred. No. 7.2e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ANSFVGTAYVSPPELL 16
Db 242 ANSFVGTAYVSPPELL 257

RESULT 15
Q4S4R0 TETNG PRELIMINARY; PRT; 558 AA.
AC Q4S4R0
DT 19-JUN-2005, integrated into UniProtKB/TrEMBL.
DT 19-JUN-2005, sequence version 1.
DT 07-FEB-2006, entry version 5.
DE Chromosome 2 SCAP14738, whole genome shotgun sequence. (Fragment).
GN ORFNames=GSTENG0024075001;
OS Tetradon nigriviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodon.
OC NCBI_TaxId=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15496914; DOI=10.1038/nature03025;
RA Jaillon O., Aury J.-M., Brunet F., Petit J.-L., Stange-Thomann N.,
RA Maucell E., Bouneau L., Fischer C., Ozouf-Coetzac C., Bernot A.,
RA Niclaud S., Jaffe D., Fisher S., Lutfalla G., Dosat C., Segurens B.,
RA Daelva C., Salenoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA Blomont C., Skalli Z., Carotico L., Poulat J., De Bernardis V.,
RA Ctraud C., Duprat S., Broctier P., Coutanceau J.-P., Gouzy J.,
RA Parra G., Lardier G., Chappie C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Volff J.-N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Winkler P., Lander B.S., Weissbach J., Roest Crolius H.;
RT "Genome duplication in the teleost fish Tetradon nigriviridis reveals
RT the early vertebrate proto-karyotype.";
RL Nature 431:946-957(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RG Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -1- FUNCTION: Plays a key role in the control of the eukaryotic cell
CC cycle. It is required in higher cells for entry into S-phase and
CC mitosis. Component of the kinase complex that phosphorylates the
CC repetitive C-terminus of RNA polymerase II. Catalytic component of
CC MPF (By similarity).
CC -1- SUBUNIT: Forms a stable but non-covalent complex with cyclin B in

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CC      mature oocytes (By similarity).
CC      -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
CC      -----
CC      Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC      Distributed under the Creative Commons Attribution-NonDeriv License
CC      -----
DR      EMBL, CAAB01014738; CAG04372.1; -, Genomic_DNA.
DR      SMR, Q4S4R0; 78-364, 417-557.
DR      GO, GO:0005524; F:ATP binding; IEA.
DR      GO, GO:0000166; F:nucleotide binding; IEA.
DR      GO, GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR      GO, GO:0016740; F:transferase activity; IEA.
DR      GO, GO:0006468; P:protein amino acid phosphorylation; IEA.
DR      InterPro, IPR000719; Prot_Kinase.
DR      InterPro, IPR008271; Ser_Thr_pkin_AS.
DR      InterPro, IPR002290; Ser_Thr_pkinase.
DR      InterPro, IPR001245; Tyr_pkinase.
DR      Pfam, PF00069; Pkinase; I.
DR      ProDom, PD000001; Prot_Kinase; 1.
DR      SMART, SMO0220; S_TKC; 1.
DR      PROSITE, PS00107; PROTEIN KINASE ATP; 1.
DR      PROSITE, PS00101; PROTEIN KINASE DOM; 1.
DR      PROSITE, PS00108; PROTEIN KINASE ST; 1.
KM      ATP-binding; Kinase; Nucleotide-Binding;
KM      Serine/threonine-protein kinase; transferase.
SQ      SEQUENCE 558 AA; 63806 MW; 4E0997DA7344C73A CRC64;
QY      1 ANSFVGTAYQVYSPELL 16
DB      245 ANSFVGTAYQVYSPELL 260

RESULT 16
PDPK1 MOUSE STANDARD: PRT; 559 AA.
AC Q9Z2A0; Q9RLD8; Q9R215;
DT 18-OCT-2001, Integrated into UniProtKB/Swiss-Prot.
DT 18-OCT-2001, sequence version 2.
DT 07-MAR-2006, entry version 44.
DE 3-phosphoinositide-dependent protein kinase 1 (EC 2.7.1.37) (mPKI).
GN Name=pdpki; Synonym=pdk1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
NCBI_Taxid=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE [mRNA].
RC TISSUE=Liver;
RA Dorey L.O.; Zhang R.-B.; Langlais P.; He H.; Clark M.; Zhu L.; Liu F.;
RX Momb L.O.; Zhang R.-B.; Langlais P.; He H.; Clark M.; Zhu L.; Liu F.;
RT "Primary structure, tissue distribution, and expression of mouse
RT phosphoinositide-dependent protein kinase-1, a protein kinase that
RT phosphorylates and activates protein kinase C zeta.";
RL J. Biol. Chem. 274:8117-8122(1999).
RN [2]
RP NUCLEOTIDE SEQUENCE [mRNA].
RC TISSUE=Brain;
RA "Mouse phosphoinositide-dependent protein kinase 1 (mPKI).";
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE [mRNA].
RC STRAIN=C57BL/6;
RA Xu P.; Taylor S.;
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Phosphorylates and activates not only PKB/AKT, but also
CC PKA, PKC-zeta, p70S6K and p90S6K/RSK. May play a general role in

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CC	signaling processes and in development. Could also play a role in
CC	sex differentiation processes.
CC	-1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC	-1- SUBCELLULAR LOCATION: Cytoplasmic and membrane-associated after
CC	cell stimulation leading to its translocation. Tyrosine
CC	phosphorylation seems to occur only at the plasma membrane.
CC	-1- TISSUE SPECIFICITY: Highly expressed in heart, brain, liver and
CC	testis, also expressed in embryonic cells.
CC	-1- PTM: Phosphorylated on tyrosine and serine/threonine.
CC	Phosphorylation on Ser-244 in the activation loop is required for
CC	full activity. PDKI itself can autophosphorylate Ser-244, leading
CC	to its own activation (By similarity).
CC	-1- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PDKI
CC	subfamily.
CC	-1- SIMILARITY: Contains 1 PH domain.
CC	-----
CC	Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC	Distributed under the Creative Commons Attribution-NoDerivs license
CC	-----
CC	EMBL; AF086625; AAC67544.1; -; mRNA.
DR	EMBL; AF126294; AAD38505.1; -; mRNA.
DR	EMBL; AF079535; AAC96115.1; -; mRNA.
DR	HSSP; O15530; H1M.
DR	SMR; Q9Z2A0; 75-361, 412-559.
DR	InAct; Q9Z2A0; -.
DR	Ensembl; ENSMUSG00000024122; Mus musculus.
DR	MG1; MG1; I338068; Pdk1.
DR	GO; GO:0005737; C:cytoplasm; IDA.
DR	GO; GO:0016023; C:cytoplasmic membrane-bound vesicle; IDA.
DR	GO; GO:0004676; F:3-phosphoinositide-dependent protein kinase. .; IDA
DR	GO; GO:0006972; P:hyperosmotic response; IDA.
DR	GO; GO:0007165; P:signal transduction; TAS.
DR	InterPro; IPR011849; PH.
DR	InterPro; IPR011993; PH type.
DR	InterPro; IPR000719; Pro kinase.
DR	InterPro; IPR008271; Ser_Ehr_pkin_AS.
DR	InterPro; IPR002290; Ser_Ehr_pkinase.
DR	InterPro; IPR001245; Tyr_pkinase.
DR	Pfam; PF00069; Pkinase; 1.
DR	ProDom; PD000001; Prot kinase; 1.
DR	SMART; SM00220; S_TKc; 1.
DR	PROSITE; PSS0003; PH_DOMAIN, FALSE_NEG.
DR	PROSITE; PSS00107; PROTEIN_KINASE_ATP; 1.
DR	PROSITE; PSS0011; PROTEIN_KINASE_DOM; 1.
DR	PROSITE; PS00108; PROTEIN_KINASE_SF; 1.
KW	ATP-binding; Kinase; Membrane; Nucleotide-binding; Phosphorylation;
KW	Serine/threonine-protein kinase; Transferase
FT	CHAIN
FT	1 559
FT	FT
FT	DOMAIN
FT	85 345
FT	DOMAIN
FT	462 553
FT	NP_BIND
FT	91 99
FT	COMPBIAS
FT	392 401
FT	ACT_SITE
FT	208 208
FT	BINDING
FT	114 114
FT	MOD_RES
FT	9 9
FT	MOD_RES
FT	25 25
FT	MOD_RES
FT	244 244
FT	FT
FT	MOD_RES
FT	376 376
FT	MOD_RES
FT	379 379
FT	MOD_RES
FT	396 396
FT	MOD_RES
FT	399 399
FT	MOD_RES
FT	406 406
FT	MOD_RES
FT	413 413
FT	CONFLICT
FT	84 84
FT	CONFLICT
FT	248 248
FT	CONFLICT
FT	285 285
FT	CONFLICT
FT	546 546
FT	SEQUENCE
FT	559 AA; 63759 MW; F2A617A27460FAC9 CRC64;
Query Match	100.0%; Score 79; DB 1; Length 559;

Best Local Similarity 100.0%; Pred. No. 7.3e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ANSFVGTAGYVSPPELL 16
Db 242 ANSFVGTAGYVSPPELL 257

RESULT 17
PDPK1_RAT STANDARD; PRT; 559 AA.

AC 055173;
DT 18-OCT-2001, integrated into UniProtKB/Swiss-Prot.
DT 01-JUN-1998, sequence version 1.
DT 07-MAR-2006, entry version 42.
DE 3-phosphoinositide-dependent protein kinase 1 (EC 2.7.1.37) (Protein
kinase B kinase) (PKB kinase).
GN Name=Pdk1; Synonyms=pdk1;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RC TISSUE=Brain;
RX MEDLINE=98111410; PubMed=9445477; DOI=10.1126/science.279.5351.710;
RA Stephens L.R., Anderson K.E., Stokoe D., Erdjument-Bromage H.,
Painter G.F., Holmes A.B., Gaffney P.R.J., Reese C.B., McCormick F.,
Temper P., Coadwell W.J., Hawkin P.T.;
RT "Protein kinase B kinases that mediate phosphatidylinositol 3,4,5-
triphosphate-dependent activation of protein kinase B.";
RL Science 279:710-714(1998).
CC -!- FUNCTION: Phosphorylates and activates not only PKB/AKT, but also
PKA, PKC-zeta, p70S6K and p90S6K/RSK. May play a general role in
signaling processes and in development (By similarity).
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic and membrane-associated after
cell stimulation leading to its translocation. Tyrosine
phosphorylation seems to occur only at the plasma membrane (By
similarity).
CC -!- PPM: Phosphorylated on tyrosine and serine/threonine.
CC Phosphorylation on Ser-244 in the activation loop is required for
full activity. PDK1 itself can autophosphorylate Ser-244, leading
to its own activation (By similarity).
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PDK1
subfamily.
CC -!- SIMILARITY: Contains 1 PH domain.
CC -----
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NonDerivs License
CC -----
DR EMBL: Y15748; CAA75758.1; -; mRNA.
DR HSSP: O15530; 1H1W.
DR SMR: O55173; 75-361, 412-559.
DR Ensembl: ENSRNOG00000006136; Rattus norvegicus.
DR RSD: 620307; Pdk1.
DR InterPro: IPR001849; PH.
DR InterPro: IPR011993; PH type.
DR InterPro: IPR000719; Prot kinase.
DR InterPro: IPR008271; Ser Thr pkin AS.
DR InterPro: IPR002290; Ser_Thr_kinase.
DR InterPro: IPR001245; Tyr_kinase.
DR Pfam: Pf00069; Pkinase; 1.
DR ProDom: PD000001; Prot kinase; 1.
DR SMART: SMO0220; S_TKc; 1.
DR PROSITE: PSS0003; PH DOMAIN; FALSE NEG.
DR PROSITE: PSS0107; PROTEIN KINASE ATP; 1.
DR PROSITE: PSS0011; PROTEIN KINASE_DOM; 1.
DR PROSITE: PSS0108; PROTEIN KINASE_ST; 1.
DR ATP-binding; Kinase; Membrane; Nucleotide-binding; Phosphorylation;
KM Serine/threonine-protein kinase; Transferase.
FT CHAIN 1 559 3-phosphoinositide-dependent protein

FT FT Kinase 1.
FT FT /FTID=PRO_0000086502.
FT FT DOMAIN 85 345
FT FT PH. 462 353
FT FT NP_BIND 91 99
FT FT COMPBIAS 392 399
FT FT ACT_SITE 208 208
FT FT BINDING 114 114
FT FT MOD_RES 9 9
FT FT MOD_RES 25 25
FT FT MOD_RES 244 244
FT FT MOD_RES 376 376
FT FT MOD_RES 379 379
FT FT MOD_RES 396 396
FT FT MOD_RES 399 399
FT FT MOD_RES 406 406
FT FT MOD_RES 413 413
SQ SEQUENCE 559 AA; 63609 MW; ADE70A7F6C2A20BF CRC64;
Query Match Score 79; DB 1; Length 559;
Best Local Similarity 100.0%; Pred. No. 7.3e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ANSFVGTAGYVSPPELL 16
Db 242 ANSFVGTAGYVSPPELL 257

RESULT 18
ID QJUNG6_MOUSE PRELIMINARY; PRT; 559 AA.
AC QJUNG6;
DT 11-OCT-2005, integrated into UniProtKB/TrEMBL.
DT 21-FEB-2006, entry version 8.
DE Melanocyte cDNA, RIKEN full-length enriched library, clone:G27062J02
DE product:3-phosphoinositide dependent protein kinase-1, full insert
DE sequence.
GN Name=Pdk1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J;
RX MEDLINE=9279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.,
RT "High-efficiency full-length cDNA cloning.";
RL Methods Enzymol. 303:19-44(1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J;
RX PubMed=16141072; DOI=10.1126/science.1112014;
RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
Davis M.J., Wilmink L.G., Altinis J., Allen J.E.,
Ambesi-Impombato A., Apweiler R., Aturaliya R., Avramovic M.,
Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
Chiu K.P., Choudhary V., Christofels A., Clutterbuck D.R.,
Crowe M.V., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
di Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G.,
Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
Gastrolin-Hemling P., Gingeras T.R., Gojobori T., Green R.E.,
Guertlich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
Hilli D., Huhmrich L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kello J., Kitamura H.,
Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
Lluni S., McMillan S., Madan Babu M., Madera M., Marchionni L.,

RA Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
 RA Mottagui-Farab S., Mulder N., Nakano N., Nakanishi H., Ng P.,
 RA Nilsen R., Nishiguchi S., Nishikawa S., Noji F., Ohara O.,
 RA Okazaki Y., Oriando V., Pang K.C., Pavan W.J., Pavese G.,
 RA Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
 RA Roet B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
 RA Schonbach C., Seifguchi K., Sempke C.A., Sero S., Sessa L., Sheng Y.,
 RA Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
 RA Sperling S., Stupka E., Sugita K., Sultana R., Takenaka Y., Taki K.,
 RA Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
 RA Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yaqui K.,
 RA Yamashita H., Zabarovsky E., Zhu S., Zimmer A., Hide M., Bult C.,
 RA Grimmer S.M., Teasdale R.D., Liu B.T., Brusic V., Quackenbush J.,
 RA Walstedt C., Wattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
 RA Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
 RA Iida J., Imanura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
 RA Kawashima T., Kojima M., Kondo S., Kono H., Nakano K., Niimura N.,
 RA Nishio T., Okada M., Plessey C., Shibata K., Shiraki T., Suzuki S.,
 RA Tagami M., Waki K., Watanabe A., Okamura-Oho Y., Suzuki H., Kawai J.,
 RA Hayashizaki Y.,
 RA "The transcriptional landscape of the mammalian genome.",
 RA Science 309:1559-1563 (2005).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J;
 RX PubMed=16141073; DOI=10.1126/science.1112009;
 RG RIKEN Genome Exploration Research Group, and Genome Science Group
 (Genome Network Core Team) and the FANTOM Consortium;
 RT "Antisense Transcription in the Mammalian Transcriptome.",
 RL Science 309:1564-1566 (2005).
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J;
 RX MEDLINE=223554683; PubMed=12466851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nikaido I., Osato N., Saito R., Suzuki H., Yamana I., Kiyosawa H.,
 RA Yaqui K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gotohori T.,
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schirml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
 RA Blake J.A., Brad D., Brusic V., Chochia C., Corbani L.E., Cousins S.,
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
 RA Grimmond S., Guertincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kanai A., Kawai H., Kawasawa Y., Kedzierski R.M., King B.L.,
 RA Kanagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA MacIsaac D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Petosa G., Pesole G.,
 RA Petrovsky N., Piliat R., Pontius J.U., Qi D., Ramchandran S.,
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Sandelin A., Schneider C., Sempke C.A., Setou M., Shimada K.,
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
 RA Verardo R., Wagner L., Walstedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wilming L.G., Wyshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
 RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 RA Hirozane-Kishikawa T., Kono H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
 RA Yamashita A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.,
 RA "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.",
 RL Nature 420:563-573 (2002).
 RN [5]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana I.,
 RA Saito T., Okazaki Y., Gotohori T., Bono H., Kanagawa T., Saito R.,
 RA Kaotaka K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,

RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schirml L.M., Straubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barch G.,
 RA Blake J., Boffelli D., Bojuna N., Carninci P., de Bernaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Guertincich S., Hill D., Hofmann M., Hume D.A., Kanlaya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima S., Mazzei J., Mombert P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weltz C., Whitaker C., Wilming L.,
 RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
 RA Hayashizaki Y.,
 RA "Functional annotation of a full-length mouse cDNA collection.",
 RL Nature 409:685-690 (2001).
 RN [6]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J;
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.,
 RA "Normalisation and subcloning of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes.",
 RL Genome Res. 10:1617-1630 (2000).
 RN [7]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagasaka S., Sasaki N., Carninci P.,
 RA Kono H., Akiyama Y., Nishi K., Kitanaka T., Tashiro H., Itoh M.,
 RA Suni N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kasliwagi K.,
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanabe M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
 RA "RIKEN integrated sequence analysis (RISA) system-384 format
 RT sequencing pipeline with 384 multicapillary sequencer.",
 RL Genome Res. 10:1757-1771 (2000).
 RN [8]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J;
 RA Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,
 RA Horii F., Iida J., Imanura K., Imotani K., Itoh M., Kanagawa S.,
 RA Kawai J., Kojima M., Kono H., Murata M., Nakamura M., Niimura N.,
 RA Nishiyori H., Nomura K., Ono M., Sakazume N., Sano H., Sasaki D.,
 RA Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watanabe A.,
 RA Muramatsu M., Hayashizaki Y.,
 RA Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
 CC -----
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 CC Distributed under the Creative Commons Attribution-NonDerivs license
 CC -----
 CC EMBL: AK147835; BAE28171.1; -, mRNA.
 CC MG1: MG1:338068; Pdpk1.
 DR GO: GO:0005737; C:cytoplasmic, IDA.
 DR GO: GO:0016023; C:cytoplasmic membrane-bound vesicle, IDA.
 DR GO: GO:0004676; F:3-phosphoinositide-dependent protein kinase. . . IDA.
 DR GO: GO:0006972; P:hydropotomotic response, IDA.
 DR GO: GO:0007165; P:signal transduction; TAS.
 DR InterPro: IPR000719; Prot_kinase.
 DR InterPro: IPR008271; Ser_thr_kinase.
 DR InterPro: IPR002290; Ser_thr_kinase.
 DR InterPro: IPR001245; Tyr_kinase.
 DR Pfam: PF00069; Pkinase; 1.
 DR ProDom: PD000001; Prot_kinase; 1.
 DR SMART: SM00220; S_TKc_1.
 DR PROSITE: PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE: PS50011; PROTEIN KINASE DOM; 1.
 DR PROSITE: PS00108; PROTEIN KINASE ST; 1.
 KW ATP-binding; Kinase; Nucleotide-binding;
 KW Serine/threonine-protein kinase; Transferase.
 KW SEQUENCE 559 AA; 63687 MW; 7461D027460FAC CRC64;

Query Match 100.0%; Score 79; DB 2; Length 559;
 Best Local Similarity 100.0%; Pred. No. 7.3e-05;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ANSFVGTAGTVPSPLL 16
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 Db 242 ANSFVGTAGTVPSPLL 257

RESULT 19
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 AC Q3UH20;
 DT 11-OCT-2005, integrated into UniProtKB/TrEMBL.
 DT 11-OCT-2005, sequence version 1.
 DT 21-FEB-2006, entry version 8.
 DE cDNA, RIKEN full-length enriched library, clone:192018K11 product:3-phosphoinositide dependent protein kinase-1, full insert sequence.
 GN Name=dpk1;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Muridae; Murinae; Mus.
 NCBI Taxid=10090;
 [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.,
 RT "High-efficiency full-length cDNA cloning.",
 RL Methods Enzymol. 303:19-44(1999).
 [2]
 RP NUCLEOTIDE SEQUENCE.
 RX PubMed=16141072; DOI=10.1126/science.1112014;
 RA Carninci P., Kaubkawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
 RA Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
 RA Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
 RA Davis M.J., Wilmong L.G., Altshuler E., Allen J.E.,
 RA Ambesi-Impombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
 RA Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
 RA Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
 RA Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
 RA di Bernarado C.F., Down T., Engstrom P., Fagioli M., Gariboldi M.,
 RA Fletcher C.P., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
 RA Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
 RA Guignard L., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
 RA Hill D., Hummelbeck L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
 RA Jakt M., Kanapin A., Katoh M., Kawagawa Y., Kelso J., Kitamura H.,
 RA Kitano H., Kollas G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
 RA Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
 RA Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
 RA Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
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 RA Natsugai R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
 RA Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavoni G., Pesole G.,
 RA Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
 RA Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
 RA Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,
 RA Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
 RA Sperling S., Stupka E., Sugita K., Sultana R., Takenaka Y., Taki K.,
 RA Tamajima K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
 RA Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
 RA Yamamoto S., Zabarovsky B., Zhu S., Zimmer A., Hilde W., Bult C.,
 RA Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
 RA Mahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
 RA Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki Y., Arakawa T.,
 RA Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawaguchi N.,
 RA Kawashima T., Kojima M., Kondo S., Kono H., Nakano K., Niimura N.,
 RA Nishio T., Okada M., Plessey C., Shibata K., Shiraki T., Suzuki S.,
 RA Teyam M., Waki K., Watanabe A., Okamura-Oho Y., Suzuki H., Kawai J.,
 RT "The transcriptional landscape of the mammalian genome.",
 RL Science 309:1559-1563(2005).

RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RX PubMed=16141073; DOI=10.1126/science.1112009;
 RA RIKEN Genome Exploration Research Group, and Genome Science Group
 RG (Genome Network Core Team) and the PANTOM Consortium,
 RT "Antisense transcription in the Mammalian Transcriptome.",
 RL Science 309:1564-1566(2005).
 [4]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kaubkawa T., Adachi J., Bono H., Kondo S.,
 RA Nikaido I., Osato N., Saito R., Suzuki H., Yamana I., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schirml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
 RA Blake J.A., Brad D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
 RA Dalla E., Dragani T.A., Fletcher C.P., Forrest A., Gough J.,
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
 RA Grimmond S., Guenrich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kanai A., Kawaji H., Kawagawa Y., Kedzierski R.M., King B.L.,
 RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Pereira G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramchandran S.,
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Saitana R., Schneider C., Semple C.A., Setou M., Shimada K.,
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
 RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wilmong L.G., Wyshnaw-Boris A., Yanagisawa M., Yang I., Yang L.,
 RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 RA Hirozane-Kikukawa T., Kono H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shimokawa A.,
 RA Yamanashi A., Yoshino M., Watanabe R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.,
 RT "Analysis of the mouse transcriptome based on functional annotation of
 60,770 full-length cDNAs.",
 RL Nature 420:563-573(2002).
 [5]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana I.,
 RA Saito K., Okazaki Y., Gojobori T., Bono H., Kaubkawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schirml L.M., Staudl F., Suzuki R., Tomita M., Wagner L., Watanabe Y.,
 RA Sakai K., Okido T., Furuno M., Bono H., Baldarelli R., Barab G.,
 RA Blake J., Botfield D., Bojunga N., Carninci P., de Bono B., M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Guignard L., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima T., Mazzarelli J., Mombauts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schonbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki K., Toyooka K., Wang K.H., Weller C., Whitaker C., Wilmong L.,
 RA Wyshnaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
 RT "Functional annotation of a full-length mouse cDNA collection.",
 RL Nature 409:685-690(2001).
 [6]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.,
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new genes.",
 RL Genome Res. 10:1617-1630(2000).
 [7]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;


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RA Shibata K., Itch M., Aizawa K., Nagaoaka S., Sasaki N., Carninci P.,
RA Komno H., Akiyama J., Nishi K., Katsunai T., Teshiro H., Itch M.,
RA Suni N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kasahigaki K.,
RA Fujiwaka S., Inoue K., Ozawa Y., Izawa M., Ohara E., Watanabe M.,
RA Yoneda Y., Ishikawa T., Ogawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
RA "Riken integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [8]
RP NUCLEOTIDE SEQUENCE.
RA Arkawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,
RA Hori F., Iida U., Imamura K., Imotani K., Itch M., Kanagawa S.,
RA Kawai J., Kojima M., Komno H., Murata M., Nakamura M., Ninomiya N.,
RA Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D.,
RA Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watanabe A.,
RA Muramatsu M., Hayashizaki Y.
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
CC -----
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CC -----
DR EMBL: AK147149; BA27716.1; -, mRNA.
DR MGI: MGI:1338068; Pdpk1.
DR GO: GO:0005737; C:cytoplasm; IDA.
DR GO: GO:0004676; F:3-phosphoinositide-dependent vesicle; IDA.
DR GO: GO:0004676; F:3-phosphoinositide-dependent protein kinase. . . IDA.
DR GO: GO:0006972; P:hyperosmotic response; IDA.
DR GO: GO:0007165; P:signal transduction; TAS.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR008271; Ser_thr_pkin_AS.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR InterPro: IPR001245; Tyr_pkinase.
DR Pfam: PF00069; Pkinase; 1.
DR ProDom: PD000001; Prot_kinase; 1.
DR SMART: SM00220; S_TKC; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS0011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
DR ATP-binding; Kinase; Nucleotide-Binding;
KW Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 559 AA; 63729 MW; F0D6AD27161F6B8 CRC64;

Query March 100.0%; Score 79; DB 2; Length 559;
Best Local Similarity 100.0%; Pred. No. 7.3e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ANSFVGTAAQVSPPELL 16
DB 242 ANSFVGTAAQVSPPELL 257

RESULT 20
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ID Q76BX2 ASTPE PRELIMINARY; PRT; 571 AA.
AC Q76BX2;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 21-FEB-2006, entry version 15.
DE Phosphoinositide dependent kinase-1.
GN Name=PKD1;
OS Ascarina pectinifera (Starfish).
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Asterozoa;
OC Ascidacea; Valvatacea; Valvatida; Ascidinidae; Ascidina.
OX NCBI_TaxID=7594;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Hiraoka D., Hori S., Fukuhara T., Tachibana K., Okumura E.,
RA Kishimoto T.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.

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CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
CC -----
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CC -----
DR EMBL: AB110536; BAD02370.1; -, mRNA.
DR HSSP: 063450; 1A06.
DR SMK: Q76BX2; 109-393.
DR GO: GO:0005524; F:ATP binding; IEA.
DR GO: GO:0000166; F:nucleotide binding; IEA.
DR GO: GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO: GO:0016740; F:transferase activity; IEA.
DR GO: GO:0006458; P:protein amino acid phosphorylation; IEA.
DR InterPro: IPR011993; Ph_type.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR008271; Ser_thr_pkin_AS.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR InterPro: IPR001245; Tyr_pkinase.
DR Pfam: PF00069; Pkinase; 1.
DR ProDom: PD000001; Prot_kinase; 1.
DR SMART: SM00220; S_TKC; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS0011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
DR ATP-binding; Kinase; Nucleotide-Binding;
KW Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 571 AA; 65194 MW; E65A142D69119287 CRC64;

Query March 100.0%; Score 79; DB 2; Length 571;
Best Local Similarity 100.0%; Pred. No. 7.4e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ANSFVGTAAQVSPPELL 16
DB 274 ANSFVGTAAQVSPPELL 289

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AC O6CT14;
DT 16-AUG-2004, integrated into UniProtKB/TrEMBL.
DT 16-AUG-2004, sequence version 1.
DT 21-FEB-2006, entry version 19.
DE Similar to sp|Q12336 Saccharomyces cerevisiae YOL100w PKH2.
GN OrderedLocusNames=KLUA0C12485g;
OS Kluyveromyces fragilis (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
OX NCBI_TaxID=28985;
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RP NUCLEOTIDE SEQUENCE (LARGE SCALE GENOMIC DNA).
RP STRAIN=CBS 2259 / IFO 1267 / NRRL Y-1140 / WM37;
RX PubMed=15229592; DOI=10.1038/nature02579;
RA Dujon B., Sherman D., Fischer G., Durieux P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marck C., Neuvéglise C., Talla E.,
RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Babe V.,
RA Barney S., Blanchin S., Beckerich J.-M., Bayne E., Bleykasten C.,
RA Boisarame A., Boyer J., Catolico L., Confaiolieri F., de Daruvar A.,
RA Despons L., Fabre E., Faithhead C., Ferry-Dumazet H., Groppi A.,
RA Hanttraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
RA Kerrast A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA Nicard J.-M., Nikolski M., Orzas S., Ozier-Kalogeropoulos O.,
RA Pellenz S., Potier S., Richard G.-F., Straub M.-L., Suleau A.,
RA Swennen D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA Zenlou-Meyer M., Zivanovic V., Bolotin-Fukuhara M., Thierly A.,
RA Bouchier C., Caudron B., Scarpelli C., Gallardin C., Weissenbach J.,
RA Wincker P., Souciet J.-L.;
RT "Genome evolution in yeasts.";
RL Nature 430:35-44(2004).
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
CC -----

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DR EMBL, CR382123; CAH01606.1; -; Genomic DNA.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR InterPro; IPR001849; PH.
 DR InterPro; IPR001993; PH_type.
 DR InterPro; IPR000719; Prot_Kinase.
 DR InterPro; IPR008271; Ser_Thr_pkin_AS.
 DR InterPro; IPR002290; Ser_Thr_pkinase.
 DR InterPro; IPR001245; Tyr_pkinase.
 DR Pfam; PF000169; PH; 1.
 DR Pfam; PF000069; Kinase; 1.
 DR ProDom; PD000001; Prot_Kinase; 1.
 DR SMART; SM00220; S_TKC; 1.
 DR SMART; SM00223; PH; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 DR ATP-binding; Complete proteome; Kinase; Nucleotide-binding;
 KW Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 925 AA; 103643 MW; 197FC988436B01DA CRC64;

Query Match 92.4%; Score 73; DB 2; Length 925;
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Qy 1 ANSFVGTQAYVSPPELL 16
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 Db 320 SNSFVGTAEYVSPPELL 335

RESULT 22
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 AC Q5B8M0;
 DT 26-APR-2005, integrated into UniProtKB/TrEMBL.
 DT 26-APR-2005, sequence version 1.
 DT 07-MAR-2006, entry version 13.
 DE Hypothetical protein.
 GN ORFNames=AN3110.2;
 OS Aspergillus nidulans FGSC A4.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Eutriales; Trichocomaceae; Emericella.
 OX NCBI_TaxID=227321;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=FGSC 4;
 RX PubMed=15372000; DOI=10.1038/nature04341;
 RA Galagan J.E., Calvo S.E., Cuomo C., Ma L.-J., Wortman J.R.,
 RA Kapitonov V., Lee S.-I., Baccarini M., Spevak C.C., Clutterbuck J.,
 RA Kapatczyn V., Jurka J., Saczko C., Farman M., Butler J.,
 RA Purcell S., Harris S., Braus G.H., Drah O., Busch S., D'Entfer C.,
 RA Bouchier C., Goldman G.H., Bell-Pedersen D., Griffiths-Jones S.,
 RA Doonan J.H., Yu J., Vlenken K., Pain A., Freitag M., Selker E.U.,
 RA Archer D.B., Penalva M.A., Oakley B.R., Momany M., Tanaka T.,
 RA Kadick M., Hynes M., Paolacci M., Fischer R., Miller B.L., Dyer P.S.,
 RA Sachs M.S., Osmari S.A., Birren B.W.;
 RA "Sequencing of Aspergillus nidulans and comparative analysis with A.
 RT fumigatus and A. oryzae";
 RL Nature 438:1105-1115(2005).
 CC -1- FUNCTION: Serine/threonine protein kinase probably involved in the
 CC cytoplasm to vacuole transport (Cvt) and in autophagy, where it
 CC may be required for the formation of autophagosomes (By
 CC similarity).
 CC -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 CC -1- SUBCELLULAR LOCATION: Cytoplasm (By similarity).
 CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.

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 CC -----

DR EMBL, AACD01000051; EAA63681.1; -; Genomic DNA.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0000166; F:nucleotide binding; IEA.
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0006914; F:autophagy; IEA.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR GO; GO:0015031; P:protein transport; IEA.
 DR InterPro; IPR000719; Prot_Kinase.
 DR InterPro; IPR008271; Ser_Thr_pkin_AS.
 DR InterPro; IPR002290; Ser_Thr_pkinase.
 DR InterPro; IPR001245; Tyr_pkinase.
 DR Pfam; PF00069; Kinase; 1.
 DR SMART; SM00220; S_TKC; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 DR ATP-binding; Autophagy; Hypothetical protein; Kinase;
 KW Nucleotide-binding; Protein transport;
 KW Serine/threonine-protein kinase; Transferase; Transport.
 SQ SEQUENCE 813 AA; 88969 MW; 4867152C42B10328 CRC64;

Query Match 89.9%; Score 71; DB 2; Length 813;
 Best Local Similarity 87.5%; Pred. No. 0.0028;
 Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ANSFVGTQAYVSPPELL 16
 :|||||:|||||
 Db 423 ASSFVGTAEYVSPPELL 438

RESULT 23
 Q4MYD7 ASPFU PRELIMINARY; PRT; 839 AA.
 ID Q4MYD7 ASPFU
 AC Q4MYD7;
 DT 05-JUL-2005, integrated into UniProtKB/TrEMBL.
 DT 05-JUL-2005, sequence version 1.
 DT 07-MAR-2006, entry version 11.
 DE Serine/threonine protein kinase, putative.
 GN ORFNames=AfU3g12670;
 OS Aspergillus fumigatus (Sartorya fumigata).
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Eutriales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
 OX NCBI_TaxID=5085;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=Af293 / CBS 101355 / FGSC A1100;
 RX PubMed=15372009; DOI=10.1038/nature04352;
 RA Nierman W.C., Pain A., Anderson M.J., Wortman J.R., Kim H.S.,
 RA Arroyo J., Bertram M., Abe K., Archer D.B., Bernejo C., Bennett J.W.,
 RA Bowyer P., Chen D., Collins M., Coulson R., Davies R., Dyer P.S.,
 RA Farman M., Fedorova N., Fedorova N.D., Feldblyum T.V., Fischer R.,
 RA Foster N., Frazer A., Garcia J.L., Garcia M.J., Goble A.,
 RA Goldman G.H., Gomi K., Griffiths-Jones S., Gwilliam R., Haas B.J.,
 RA Haas H., Harris D.E., Horiuchi H., Huang J., Humphrey S., Jimenez J.,
 RA Keller N., Khouri H., Kitamoto K., Kobayashi T., Konczak S.,
 RA Kulkarni R., Kumagai T., Lafont A., Latge J.-P., Li W., Lord A.,
 RA Lu C., Majoros W.H., May G.S., Miller B.L., Mohamoud Y., Molina M.,
 RA Monod M., Mouny I., Mulligan S., Murphy L.D., O'Neill S., Paulsen I.,
 RA Penalva M.A., Pertea M., Price C., Pritchard B.L., Quail M.A.,
 RA Rabinowitz E., Rawlin N., Rajandream M.A., Reichard U.,
 RA Renaud H., Robson G.D., Rodriguez de Cordoba S., Rodriguez-Pena J.M.,
 RA Ronning C.M., Ruter S., Salzberg S.L., Sanchez M.,
 RA Sanchez-Ferrero J.C., Saunders D., Seeger K., Squares R., Squares S.,
 RA Takeuchi M., Tekala F., Turner G., Vazquez de Aldana C.R., Weidman J.,
 RA White O., Woodward J.R., Yu J.-H., Frazer C.W., Galagan J.E., Asai K.,
 RA "Genomic sequence of the pathogenic and allergenic filamentous fungus
 RT Aspergillus fumigatus";

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RL Nature 438:1151-1156(2005).
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
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CC -----
DR EMBL: AAH0100002; EAL92316.1; -; Genomic_DNA.
DR GO: GO:0005524; P:ATP binding; IEA.
DR GO: GO:0000166; F:nucleotide binding; IEA.
DR GO: GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO: GO:0016740; F:transferase activity; IEA.
DR GO: GO:0006914; P:autophagy; IEA.
DR GO: GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR008271; Ser_thr_pkin_AS.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR InterPro: IPR001245; Tyr_pkinase.
DR Pfam: PF00069; Pkinase; 1.
DR ProDom: PD000001; Prot_kinase; 1.
DR SMART: SM00220; S_TKc; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
DR KATP-binding; Complete proteome; Kinase; Nucleotide-binding;
DR Serine/threonine-protein kinase; Transferase.
DR KMW SEQUENCE 839 AA; 9218 MW; FA8587980040CABC CRC64;
SQ
Query March 89.9%; Score 71; DB 2; Length 839;
Best Local Similarity 87.5%; Pred. No. 0.0029;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 ANSFVGTAAQVSPPELL 16
Db 445 ASSFVGTAEVSPPELL 460

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CC -----
DR EMBL: AP007161; BAB0968.1; -; Genomic_DNA.
DR KATP-binding; Kinase; Nucleotide-binding;
DR Serine/threonine-protein kinase; Transferase.
DR KMW SEQUENCE 850 AA; 9295 MW; 42FDC3F9CE3267M4 CRC64;
SQ
Query March 89.9%; Score 71; DB 2; Length 850;
Best Local Similarity 87.5%; Pred. No. 0.0029;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 ANSFVGTAAQVSPPELL 16
Db 456 ASSFVGTAEVSPPELL 471

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KM ATP-binding; Complete proteome; Kinase; Nucleotide-binding;
 KW Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 1542 AA; 166981 MW; 6385C2BC9FC0E169 CRC64;
 Query Match 89.9%; Score 71; DB 2; Length 1542;
 Best Local Similarity 87.5%; Pred. No. 0.0053;
 Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 NSFVGTAGVSPPELL 16
 DB 823 AHSEVGTAEVSPPELL 838

RESULT 26
 OS4TW2 DICTDI
 ID Q54TW2 DICTDI PRELIMINARY; PRT; 686 AA.
 AC Q54TW2;
 DT 24-MAY-2005, integrated into UniProtKB/TrEMBL.
 DT 24-MAY-2005, sequence version 1.
 DT 21-FEB-2006, entry version 10.
 DE Hypothetical protein DDB0216243.
 GN Name=DDB0216243; ORFNames=DDB0216243;
 OS Dictyostelium discoideum (Slime mold).
 OC Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.
 OX NCBI_TaxID=44689;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=AK4;
 RX PubMed=15875012; DOI=10.1038/nature03481;
 RA Eichinger L., Pachbat J.A., Gloeckner G., Rajandream M.A.,
 RA Sussang R., Berriman M., Song J., Olsen R., Szafarski K., Xu Q.,
 RA Tunggal B., Kummerfeld S., Madera M., Konfortov B.A., Riviero F.,
 RA Bankier A.T., Lehmann R., Hamlin N., Davies R., Gaudet P., Fey P.,
 RA Pilcher K., Chen G., Saunders D., Sodergren E.J., Davis P.,
 RA Kerhornou A., Nie X., Hall N., Anjard C., Hemphill L., Bason N.,
 RA Farbrother P., Desany B., Just E., Morio T., Rost R., Churcher C.M.,
 RA Cooper J., Haydock S., van Driessche N., Cronin A., Goodhead I.,
 RA Muzny D.M., Moutier T., Pain A., Lu M., Harper D., Lindsay R.,
 RA Hauser H., James K.D., Gules M., Madan Babu M., Saito T.,
 RA Buchreiter C., Wardrop A., Felder M., Thangavelu M., Johnson D.,
 RA Khalil M.A., Louie H., Mungall K.L., Oliver K., Price C.,
 RA Quail M.A., Urichihara H., Hernandez J., Rabinowitsch E., Steffen D.,
 RA Sanders M., Ma J., Kohara Y., Sharp S., Simmons M.N., Spiegler S.,
 RA Tivey A., Sugano S., White B., Walker D., Woodward J.R., Winckler T.,
 RA Tanaka Y., Shaulsky G., Schleicher M., Weinstock G.M., Rosenthal A.,
 RA Cox E.C., Chisholm R.L., Gibbs R.A., Loomis W.F., Platzer M.,
 RA Kay R.R., Williams J.G., Dear P.H., Noegel A.A., Barrell B.G.,
 RA Kuspa A.;
 RT "The genome of the social amoeba Dictyostelium discoideum";
 RL Nature 435:43-57(2005).
 CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 CC -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
 CC -----
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 CC -----
 CC EMBL: AAF10100074; EAL6717.1; -; Genomic_DNA.
 DR GO: GO:0005524; F:ATP binding; IEA.
 DR GO: GO:0000166; F:nucleotide binding; IEA.
 DR GO: GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO: GO:0016740; F:transferase activity; IEA.
 DR GO: GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR InterPro: IPR001849; Pfam.
 DR InterPro: IPR001993; Pfam type.
 DR InterPro: IPR000719; Prot kinase.
 DR InterPro: IPR008271; Ser_Thr_Pkin_AS.
 DR InterPro: IPR002290; Ser_Thr_Pkinase.
 DR InterPro: IPR001245; Tyr_kinase.
 DR Pfam: PF00069; Pkinase; 1.
 DR ProDom: PD000001; Prot_kinase; 2.

DR SMART: SM00233; Pfam; 1.
 DR SMART: SM00220; S_TKC; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 KW ATP-binding; Coiled coil; Hypothetical protein; Kinase;
 KW Nucleotide-binding; Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 686 AA; 75562 MW; C4FC7FE8539A842 CRC64;

QY 2 NSFVGTAGVSPPELL 16
 DB 346 NSFVGTAEVSPPELL 360

RESULT 27
 PKH3 ASHGO
 ID PKH3 ASHGO STANDARD; PRT; 726 AA.
 AC Q753D9;
 DT 08-NOV-2005, integrated into UniProtKB/Swiss-Prot.
 DT 05-JUL-2004, sequence version 1.
 DT 07-FEB-2006, entry version 23.
 DE Serine/threonine-protein kinase PKH3 (EC 2.7.1.37).
 GN Name=PKH3; Ordered locus Names=AFR377C;
 OS Arabidopsis thaliana (Yeast) (Eremothecium gossypii).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Eremothecium.
 OX NCBI_TaxID=33169;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=ATCC 10895;
 RX PubMed=15001715; DOI=10.1126/science.1095781;
 RA Dietrich F.S., Voegelé S., Brachat S., Lerch A., Gates K., Steiner S.,
 RA Mohr C., Poehlmann R., Luedi P., Choi S., Wing R.A., Flavler A.,
 RA Gaffney T.D., Philippsen P.;
 RT "The Arabidopsis gossypii genome as a tool for mapping the ancient
 RT Saccharomyces cerevisiae genome";
 RL Science 304:304-307(2004).
 CC -1- FUNCTION: Serine/threonine-protein kinase (By similarity).
 CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
 CC -----
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 CC -----
 CC EMBL: AEO16819; AAS53748.1; -; Genomic_DNA.
 DR HSP: Q63450; 1A06.
 DR AGD: AFR377C; -;
 DR InterPro: IPR000719; Prot_kinase.
 DR InterPro: IPR008271; Ser_Thr_Pkin_AS.
 DR InterPro: IPR002290; Ser_Thr_Pkinase.
 DR InterPro: IPR001245; Tyr_kinase.
 DR Pfam: PF00069; Pkinase; 1.
 DR ProDom: PD000001; Prot_kinase; 1.
 DR SMART: SM00220; S_TKC; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 KW ATP-binding; Complete proteome; Kinase; Nucleotide-binding;
 KW Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 726 AA; 81035 MW; 15303855D842A8E CRC64;

Query Match 88.6%; Score 70; DB 2; Length 686;
 Best Local Similarity 86.7%; Pred. No. 0.0035;
 Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 NSFVGTAGVSPPELL 16
 DB 346 NSFVGTAEVSPPELL 360

RESULT 27
 PKH3 ASHGO
 ID PKH3 ASHGO STANDARD; PRT; 726 AA.
 AC Q753D9;
 DT 08-NOV-2005, integrated into UniProtKB/Swiss-Prot.
 DT 05-JUL-2004, sequence version 1.
 DT 07-FEB-2006, entry version 23.
 DE Serine/threonine-protein kinase PKH3 (EC 2.7.1.37).
 GN Name=PKH3; Ordered locus Names=AFR377C;
 OS Arabidopsis thaliana (Yeast) (Eremothecium gossypii).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Eremothecium.
 OX NCBI_TaxID=33169;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=ATCC 10895;
 RX PubMed=15001715; DOI=10.1126/science.1095781;
 RA Dietrich F.S., Voegelé S., Brachat S., Lerch A., Gates K., Steiner S.,
 RA Mohr C., Poehlmann R., Luedi P., Choi S., Wing R.A., Flavler A.,
 RA Gaffney T.D., Philippsen P.;
 RT "The Arabidopsis gossypii genome as a tool for mapping the ancient
 RT Saccharomyces cerevisiae genome";
 RL Science 304:304-307(2004).
 CC -1- FUNCTION: Serine/threonine-protein kinase (By similarity).
 CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
 CC -----
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 CC -----
 CC EMBL: AEO16819; AAS53748.1; -; Genomic_DNA.
 DR HSP: Q63450; 1A06.
 DR AGD: AFR377C; -;
 DR InterPro: IPR000719; Prot_kinase.
 DR InterPro: IPR008271; Ser_Thr_Pkin_AS.
 DR InterPro: IPR002290; Ser_Thr_Pkinase.
 DR InterPro: IPR001245; Tyr_kinase.
 DR Pfam: PF00069; Pkinase; 1.
 DR ProDom: PD000001; Prot_kinase; 1.
 DR SMART: SM00220; S_TKC; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 KW ATP-binding; Complete proteome; Kinase; Nucleotide-binding;
 KW Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 726 AA; 81035 MW; 15303855D842A8E CRC64;

Query Match 88.6%; Score 70; DB 2; Length 726;
 Best Local Similarity 87.5%; Pred. No. 0.0037;

Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ANSFVGTAAQYVSPBL 16
 Db 174 ATSFVGTAEYVSPBL 189

RESULT 28
 OS3P6 CANAL PRELIMINARY; PRT; 944 AA.
 ID Q5A3P6; AC Q5A3P6;
 DT 26-APR-2005, integrated into UniProtKB/TrEMBL.
 DT 26-APR-2005, sequence version 1.
 DT 21-FEB-2006, entry version 13.
 DE Likely protein kinase.
 GN Name=PfK11; ORFNames=Cao19.5224;
 OS Candida albicans SC5314.
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 CC Saccharomycetales; mitosporic Saccharomycetales; Candida.
 NCBI_TaxID=237561;

RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=SC5314;
 RA Jones T., Federapfel N.A., Chibana H., Dungen J., Kalman S., Magee B.B., Newport G., Thorstenson Y.R., Agabian N., Magee P.T., Davis R.W., Scherer S.;
 RT "The diploid genome sequence of *Candida albicans*."
 RL Proc. Natl. Acad. Sci. U.S.A. 101:7329-7334(2004).
 CC -1- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is preliminary data.
 CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
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DR EMBL; AAC001000071; EAK97297.1; -; Genomic DNA.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0000166; F:nucleotide binding; IEA.
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0006914; P:autophagy; IEA.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR GO; GO:0015031; P:protein transport; IEA.
 DR InterPro: IPR000719; Prot. kinase.
 DR InterPro: IPR008271; Ser. Thr. Pkin. AS.
 DR InterPro: IPR002290; Ser. Thr. Pkinase.
 DR InterPro: IPR001245; Tyr. Pkinase.
 DR Pfam; PF00069; Pkinase; 1.
 DR SMART; SM00220; S_TKc; 1.
 DR PROSITE; PS00107; PROTEIN KINASE ATP; UNKNOWN_1.
 DR PROSITE; PS50011; PROTEIN KINASE DOM; 1.
 DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
 KW ATP-binding; Kinase; Nucleotide-binding; Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 944 AA; 106213 MW; 7451872EACE9458 CRC64;

Query March 88.6%; Score 70; DB 2; Length 944;
 Best Local Similarity 87.5%; Pred. No. 0.0048;
 Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ANSFVGTAAQYVSPBL 16
 Db 405 AKSFVGTAEYVSPBL 420

RESULT 29
 Q6BK8 DEBHA PRELIMINARY; PRT; 1062 AA.
 ID Q6BK8 DEBHA AC Q6BK8;
 DT 26-APR-2005, integrated into UniProtKB/TrEMBL.
 DT 21-FEB-2006, entry version 13.
 DE Likely protein kinase.
 GN Name=PfK11; ORFNames=Cao19.12690;

DT 21-FEB-2006, entry version 20.
 DE Similar to CA1971 CapK22 *Candida albicans* CapK22 Ser/Thr protein kinase (by homology).
 GN OrderedLocustNames=DEBA0G104179;
 OS Debaryomyces hanseni (Yeast) (*Torulaspora hanseni*).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 CC Saccharomycetales; Saccharomycetaceae; Debaryomycetes.
 NCBI_TaxID=4959;

RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RP STRAIN=ATCC 36239 / CBS 767;
 RC PubMed=15229592; DOI=10.1038/nature02579;
 RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S., Lafontaine I., de Montigny J., Marc C., Neuvéglise C., Talla B., Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V., Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C., Boissiere A., Boyer J., Cactolico L., Confiantoleri F., de Daruvar A., Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A., Hantreay F., Hennequin C., Jauniaux N., Joyet P., Kachouri R., Kerrrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H., Nicaud J.-M., Nikolski M., Ozcas S., Ozier-Kalogeropoulos O., Pellenz S., Potier S., Richard G.-F., Straub M.-L., Suleau A., Swennen D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B., Zentou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A., Bouchier C., Caudron B., Scarpelli C., Gallardin C., Weissbach J., Wincker P., Souciet J.-L.;
 RT "Genome evolution in yeasts."
 RL Nature 430:35-44(2004).
 CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
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DR EMBL; CR382139; CAG90431.1; -; Genomic DNA.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0000166; F:nucleotide binding; IEA.
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0006914; P:autophagy; IEA.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR GO; GO:0015031; P:protein transport; IEA.
 DR InterPro: IPR000719; Prot. kinase.
 DR InterPro: IPR008271; Ser. Thr. Pkin. AS.
 DR InterPro: IPR002290; Ser. Thr. Pkinase.
 DR InterPro: IPR001245; Tyr. Pkinase.
 DR Pfam; PF00069; Pkinase; 1.
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE; PS50011; PROTEIN KINASE DOM; 1.
 DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
 KW ATP-binding; Complete proteome; Kinase; Nucleotide-binding; Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 1062 AA; 117772 MW; 1FC1A34B0CF3856 CRC64;

Query March 88.6%; Score 70; DB 2; Length 1062;
 Best Local Similarity 87.5%; Pred. No. 0.0054;
 Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ANSFVGTAAQYVSPBL 16
 Db 359 AKSFVGTAEYVSPBL 374

RESULT 30
 ID Q5A3V9 CANAL PRELIMINARY; PRT; 1153 AA.
 AC Q5A3V9;
 DT 26-APR-2005, integrated into UniProtKB/TrEMBL.
 DT 21-FEB-2006, entry version 13.
 DE Likely protein kinase.
 GN Name=PfK11; ORFNames=Cao19.12690;

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OS Candida albicans SC5314.
CC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
CC Saccharomycetales; mitosporic Saccharomycetales; Candida.
CC NCBI_TaxID=237561;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=SC5314;
RX PubMed=15123810; DOI=10.1073/pnas.0401648101;
RA Jones T., Federapoli N.A., Chibana H., Dungan J., Kaiman S., P.T.,
RA Magee B.B., Newport G., Thorstenson Y.R., Agabian N., Magee P.T.,
RA Davis R.W., Scherer S.;
RT "The diploid genome sequence of Candida albicans."
RL Proc. Natl. Acad. Sci. U.S.A. 101:7329-7334(2004).
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/Genbank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
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CC -----
DR EMBL, AAC00100070; EAK97360.1; -; Genomic_DNA.
DR GO, GO:0005524; F:ATP binding; IEA.
DR GO, GO:0000166; F:nucleotide binding; IEA.
DR GO, GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO, GO:0016740; F:transferase activity; IEA.
DR GO, GO:0006914; P:autophagy; IEA.
DR GO, GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro, IPR0015031; P:protein transport; IEA.
DR InterPro, IPR000719; Prot_kinase.
DR InterPro, IPR008271; Ser_thr_pkin_AS.
DR InterPro, IPR002290; Ser_thr_pkinase.
DR InterPro, IPR001245; Tyr_pkinase.
DR Pfam, PF00069; Pkinase; 1.
DR SMART, SM00220; S_TKc; 1.
DR PROSITE, PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
DR PROSITE, PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE, PS00108; PROTEIN_KINASE_ST; 1.
DR ATP-binding; Kinase; Nucleotide-Binding;
KW Serine/threonine-protein kinase; transferase.
SQ SEQUENCE 1153 AA; 128885 MW; A331213B925F7DA3 CRC64;

Query Match 88.6%; Score 70; DB 2; Length 1153;
Best Local Similarity 87.5%; Pred. No. 0.0059;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ANSFVGTAGYVSPPELL 16
DB 405 AKSFVGTAEYVSPPELL 420

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CC -----
DR EMBL, AF294916; AAG60622.1; -; mRNA.
DR HSP, O15530; 1H1W.
DR SNR, Q9BMX6; 700-818.
DR GO, GO:0005524; F:ATP binding; IEA.
DR GO, GO:0000166; F:nucleotide binding; IEA.
DR GO, GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO, GO:0016740; F:transferase activity; IEA.
DR GO, GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro, IPR011933; PH type.
DR InterPro, IPR000215; Prot_inh_serpin.
DR InterPro, IPR008271; Ser_thr_pkin_AS.
DR InterPro, IPR002290; Ser_thr_pkinase.
DR InterPro, IPR001245; Tyr_pkinase.
DR Pfam, PF00069; Pkinase; 1.
DR SMART, SM00220; S_TKc; 1.
DR PROSITE, PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE, PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE, PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE, PS00284; SERPIN; UNKNOWN_1.
DR ATP-binding; Kinase; Nucleotide-binding;
KW Serine/threonine-protein kinase; transferase.
SQ SEQUENCE 822 AA; 90146 MW; 0BBAF8C85506AC9 CRC64;

Query Match 87.3%; Score 69; DB 2; Length 822;
Best Local Similarity 86.7%; Pred. No. 0.0063;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 NSFVGTAGYVSPPELL 16
DB 532 NSFVGTAEYVSPPELL 546

RESULT 32
ID Q4HMD3_GIBZE PRELIMINARY; PRT; 812 AA.
AC Q4HMD3;
DT 16-AUG-2005, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 7.
DE Hypothetical protein.
DE OX=NCBI_TaxID=5518;
OS Gibberella zeae (Fusarium graminearum).
CC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
CC Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
CC NCBI_TaxID=5518;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=PH-1 / NRRL 31084;
RA Birren B.W., Nuebaum C., Abouelleil A., Allen N., Anderson S.,
RA Archchi H.M., Barna N., Baetien V., Bloom T., Bogunavsky L.,
RA Boukhalter B., Butler J., Calvo S.B., Camarata J., Chang J.,
RA Choepel Y., Collymore A., Cook A., Cooke P., Corum B., Dearellano K.,
RA Diaz J.S., Dodge S., Dooley K., Dorris L., Elkins T., Engels R.,
RA Erickson J., Faro S., Ferreira P., Fitzgerald D., Gage D.,
RA Galagan J.E., Gardyna S., Gierke S., Graham L., Grand-Pierre N.,
RA Hafez N., Hagopian D., Hagos B., Hall J., Horton L., Hulme W.,
RA Iliev I., Jaffe D., Johnson R., Jones C., Kamel M., Kamat A.,
RA Karatas A., Kells C., Landers T., Levine R., Lindblad-Toh K., Liu G.,
RA Lut A., Ma L.-J., Mabbitt R., Maclean C., Macdonald P., Major J.,
RA Manning J., Matthews C., Mauceli E., McCarthy M., Meldrum J.,
RA Menues L., Mihova T., Mlenga V., Murphy T., Naylor J., Nguyen C.,
RA Nicol R., Nielsen C.B., Norbu C., O'Connor T., O'Donnell P.,
RA O'Neill D., Oliver J., Peterson K., Phunhphang P., Pierre N.,
RA Purcell S., Rachupka A., Ramsamy U., Raymond C., Retta R., Rise C.,
RA Rogov P., Roman J., Schauer S., Schniback R., Seaman S., Severy P.,
RA Smirnov S., Smith C., Spencer B., Stange-Thomann N., Stojanovic N.,
RA Stubbs M., Talamas J., Teefaye S., Theodore J., Topham K., Travers M.,
RA Vassiliev H., Venkataraman V.S., Viel R., Vo A., Wang S., Wilson B.,

```

RA Wu X., Wyman D., Young G., Zainoun J., Zemdek L., Zimmer A., Zody M.,
RA Lander E.S.,
RL "Rueartium graminearum genome sequence."
CC Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
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CC -----
CC EMBL: AAC01000447; EAA74982.1; -; Genomic_DNA.
DR GO: GO:0005524; F:ATP binding; IEA.
DR GO: GO:000166; F:nucleotide binding; IEA.
DR GO: GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO: GO:0016740; F:transferase activity; IEA.
DR GO: GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR008271; Ser_thr_pkin_AS.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR Pfam: PF00069; Pkinase; 1.
DR ProDom: PD000001; Prot_kinase; 1.
DR SMART: SM00220; S_TKc; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Complete proteome; Hypothetical protein; Kinase;
KW Nucleotide-binding; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 812 AA; 87701 MW; 356904BC73096CEF CRC64;

Query Match 86.1%; Score 68; DB 2; Length 812;
Best Local Similarity 87.5%; Pred. No. 0.0093;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Cy 1 ANSPVGTAGVYSPBL 16
Db 414 AASFVGTAEVYSPBL 429

RESULT 33
ID Q873K1_NEUCR PRELIMINARY; PRT; 922 AA.
AC Q873K1;
DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2003, sequence version 1.
DT 07-FEB-2006, entry version 19.
DE Related to 3-phosphoinositide dependent protein kinase-1 (PDK1).
GN Name=B2314.130;
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OC NCBI_TaxID=5141;
RN [1]
RA NUCLEOTIDE SEQUENCE.
RA Schulte U., Aign V., Hohelsel J., Brandt P., Fartmann B., Holland R.,
RA Nyakatura G., Mewes H.W., Mannhaupt G.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RP German Neurospora genome project;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
CC -----
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CC -----
CC EMBL: BX284746; CAD70304.1; -; Genomic_DNA.
DR HSSP: O15530; 1H1W.
DR GO: GO:0005524; F:ATP binding; IEA.
DR GO: GO:0000166; F:nucleotide binding; IEA.
DR GO: GO:0004674; F:protein serine/threonine kinase activity; IEA.

DR GO: GO:0016740; F:transferase activity; IEA.
DR GO: GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR008271; Ser_thr_pkin_AS.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR Pfam: PF00069; Pkinase; 1.
DR ProDom: PD000001; Prot_kinase; 1.
DR SMART: SM00220; S_TKc; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Nucleotide-binding;
KW Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 922 AA; 100473 MW; 0DFD2D94B81D986E CRC64;

Query Match 86.1%; Score 68; DB 2; Length 922;
Best Local Similarity 87.5%; Pred. No. 0.011;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Cy 1 ANSPVGTAGVYSPBL 16
Db 476 AASFVGTAEVYSPBL 491

RESULT 34
ID Q6FT84_CANGA PRELIMINARY; PRT; 965 AA.
AC Q6FT84;
DT 19-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 19-JUL-2004, sequence version 1.
DT 21-FEB-2006, entry version 22.
DE Similar to sp|Q12236 Saccharomyces cerevisiae YOL100w PKH2.
GN OrderedLocustNames=CAGL0G04609g;
OS Candida glabrata (Yeast) (Torulopsis glabrata).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OC NCBI_TaxID=5478;
RN [1]
RA NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RA STRAIN=ATCC 2001 / CBS 138;
RX PubMed=15229592; DOI=10.1038/nature02579;
RA Dujon B., Sherman D., Fischer G., Durans P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marck C., Nevegilise C., Talla E.,
RA Goffard N., Frangeul J., Aigle M., Anichouard V., Babour A., Barbe V.,
RA Barnay S., Blanchon S., Beckerich J.-M., Beyne E., Bleykasten C.,
RA Bolserame A., Boyer J., Cecchilico L., Confantolieri F., de Daruvar A.,
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
RA Hantraye F., Hameguin C., Jauniaux N., Joyet P., Kachouri R.,
RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA Nicaud J.-M., Nikolski M., Ozias S., Ozler-Kalogeropoulos O.,
RA Pellens S., Potier S., Richard G.-F., Straub M.-L., Suleau A.,
RA Swennen D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA Zenou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,
RA Bouchier C., Caudron B., Scarpelli C., Galliard C., Weissenbach J.,
RA Wincker P., Souciet J.-L.;
RL Nature 430:35-44(2004).
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
CC -----
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CC -----
CC EMBL: CR380953; CAG59487.1; -; Genomic_DNA.
DR GO: GO:0005524; F:ATP binding; IEA.
DR GO: GO:000166; F:nucleotide binding; IEA.
DR GO: GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO: GO:0016740; F:transferase activity; IEA.
DR GO: GO:0006468; P:protein amino acid phosphorylation; IEA.
DR GO: GO:0015031; P:protein transport; IEA.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR008271; Ser_thr_pkin_AS.

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DR InterPro: IPR002290; Ser_thr_pkinase.
DR InterPro: IPR001245; Tyr_pkinase.
DR Pfam: PF00069; Pkinase; 1.
DR ProDom: PD000001; Prot_kinase; 1.
DR SMART: SM00220; S_TKC; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
DR PROSITE: PS00108; PROTEIN_KINASE_DOM; 1.
DR ATP-binding: Complete proteome; Kinase; Nucleotide-binding;
KM Serine/threonine-protein kinase; transferase.
SQ SEQUENCE 965 AA; 108879 MW; D5B1A1D86C7517 CRC64;

Query March 86.1%; Score 68; DB 2; Length 965;
Best Local Similarity 81.2%; Pred. No. 0.011;
Matches 13; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ANSFVGTAGYVSPPELL 16
Db 286 SSSFVGTAEYVSPPELL 301

RESULT 35
Q4P4E1 USTMA PRELIMINARY; PRT; 1667 AA.
ID Q4P4E1 USTMA
AC Q4P4E1
DT 19-JUL-2005, integrated into UniProtKB/TrEMBL.
DT 19-JUL-2005, sequence version 1.
DT 21-FEB-2006, entry version 8.
DE Hypothetical protein.
GN ORFNames=UM05022.1;
OS Ustilago maydis 521.
OC Eukaryota; Fungi; Basidiomycota; Ustilaginomycetes;
OC Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago.
ON NCBI_TaxID=237631;
RX [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=521;
RA Bitren B.W., Nuebaum C., Abebe A., Aboueljelil A., Adekoya E.,
RA Alt-Zahra W., Allen N., Allen T., An P., Anderson M., Anderson S.,
RA Ateschchi H.M., Armbruster J., Bachantang P., Baldwin J., Barry A.,
RA Bayul T., Biltsheteyn B., Bloom T., Biye J., Boguslavsky L.,
RA Bowmoky M., Bouhgalter B., Brunache A., Butler J., Calixte N.,
RA Calvo S.E., Camarata J., Campo K., Chang J., Cheshtang Y.,
RA Citroen M., Collamore A., Considine T., Cook A., Cooke P., Corum B.,
RA Cuomo C., David R., Dawoe T., Degray S., Dodge S., Dooley K.,
RA Dorje P., Dorjee K., Dorris L., Duffey N., Dupes A., Elkins T.,
RA Engels R., Erickson J., Farina A., Faro S., Ferreira P., Fischer H.,
RA Fitzgerald M., Foley K., Gage D., Galagan J.E., Garin G., Gnerre S.,
RA Gutke A., Guyette A., Graham J., Grandbois E., Gyaltsen K., Hafez N.,
RA Hagopian D., Hagos B., Hall J., Hatcher B., Heller A., Higgins H.,
RA Horan T., Horn A., Houde N., Hughes L., Hulme W., Husby E., Iliev I.,
RA Jaffe D., Jones C., Kamel M., Kamat A., Kamyssele M., Karlsson E.,
RA Kells C., Klein A., Kliner P., Kodira C., Kulbokas E., Labutti K.,
RA Lama D., Landers T., Leger J., Levine S., Lewis D., Lewis T.,
RA Lindblad-Toh K., Liu X., Lokysang T., Lokysang Y., Lucien O.,
RA Lui A., Ma L.-J., Mabbitt R., MacDonald J., Maclean C., Major J.,
RA Manning J., Maraballa R., Maru K., Matthews C., Mauceli E.,
RA McCarthy M., McDonough S., McChae T., Meldrum J., Meneue L.,
RA Meitov J., Michael A., Mihova T., Mikkelson T., Mlenga V., Moru K.,
RA Moses J., Mulrain L., Munson G., Naylor J., Neves C., Nguyen C.,
RA NGUYEN N., Nguyen T., Nicol R., Nielsen C.B., Nizzari M., Norbu C.,
RA Norbu N., O'Donnell P., Okonko O., O'Leary S., Omotoho B.,
RA O'Neill K., Osman S., Parker S., Perrin D., Phunkhang P., Pigani B.,
RA Purcell S., Rachupka T., Ramasamy U., Rameau R., Ray V., Raymond C.,
RA Retta R., Richardson S., Rise C., Rodriguez J., Rogers J., Rogov P.,
RA Ruman M., Schubach R., Seaman C., Settipalli S., Sharpe T.,
RA Sheridan J., Sherpa N., Shi J., Smirnov S., Smith C., Sougnaz C.,
RA Spencer B., Stalker J., Stange-Thomann N., Stavropoulos S.,
RA Stecen K., Stone C., Stone S., Stubbs M., Talamas J., Tchunga P.,
RA Tenzing P., Testaye S., Theodore J., Thoulstang Y., Topham K.,
RA Towey S., Tsamila T., Tzomo N., Vallee D., Vassiliev H.,
RA Venkataraman V.S., Vinson J., Vo A., Wade C., Wang S., Wangchuk T.,
RA Wangdi T., Whitaker C., Wilkinson J., Wu Y., Wyman D., Yadav S.,

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RA Yang S., Yang X., Yeager S., Yee E., Young G., Zainoun J., Zembeck L.,
RA Zimmer A., Zody M., Zander E.S.;
RL "The genome sequence of Ustilago maydis."
RL Submitted (Feb-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
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CC
DR EMBL: AACP01000186; EAK85882.1; -; Genomic_DNA.
DR GO: GO:0005524; F:ATP binding; IEA.
DR GO: GO:0000166; F:nucleotide binding; IEA.
DR GO: GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO: GO:0016740; F:transferase activity; IEA.
DR GO: GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR008271; Ser_thr_pkin_AS.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR InterPro: IPR001245; Tyr_pkinase.
DR Pfam: PF00069; Pkinase; 1.
DR ProDom: PD000001; Prot_kinase; 1.
DR SMART: SM00220; S_TKC; 1.
DR PROSITE: PS00101; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
DR ATP-binding: Hypothetical protein; kinase; Nucleotide-binding;
KM Serine/threonine-protein kinase; transferase.
SQ SEQUENCE 1667 AA; 176202 MW; 9B21853249720950 CRC64;

Query March 86.1%; Score 68; DB 2; Length 1667;
Best Local Similarity 87.5%; Pred. No. 0.019;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ANSFVGTAGYVSPPELL 16
Db 1178 AASFVGTAEYVSPPELL 1193

RESULT 36
Q7PUX5 ANOGA PRELIMINARY; PRT; 484 AA.
ID Q7PUX5 ANOGA
AC Q7PUX5;
DT 15-DEC-2003, integrated into UniProtKB/TrEMBL.
DT 06-DEC-2005, sequence version 2.
DT 07-FEB-2006, entry version 17.
DE ENSANGP0000011675 (Fragment).
GN ORFNames=ENSANG00000009186;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Culicidae;
OC Anophelinae; Anopheles.
ON NCBI_TaxID=180454;
RX [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PEST;
RA The Anopheles gambiae Sequence Committee;
RT "Anopheles gambiae re-annotation."
RL Submitted (Apr-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PEST;
RA The Anopheles gambiae Sequence Committee;
RL Submitted (Apr-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
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CC
EMBL: AAB01008987; EAA00864.3; -; Genomic_DNA.

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DR GO: GO:0005524; F:ATP binding; IEA.
DR GO: GO:0000156; F:nucleotide binding; IEA.
DR GO: GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO: GO:0016740; F:transferase activity; IEA.
DR GO: GO:0006468; P:protein amino acid phosphorylation; IEA.
KW ATP-binding; Kinase; Nucleotide-binding;
KW Serine/threonine-protein kinase; Transferase.
FT NON_TER 1
FT NON_TER 484
SQ SEQUENCE 484 AA; 55700 MW; 46E98000A4B2D187 CRC64;

Query Match 84.8%; Score 67; DB 2; Length 484;
Best Local Similarity 92.9%; Pred. No. 0.0082;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SFVGTAGVSPPELL 16
Db 168 SFVGTAGVSPPELL 181

RESULT 37
Q6CPN3_KLULUA PRELIMINARY; PRT; 647 AA.
ID Q6CPN3_KLULUA
AC Q6CPN3
DT 16-AUG-2004, integrated into UniProtKB/TrEMBL.
DT 21-FEB-2006, entry version 1.
DE Similar to seq15002874 Saccharomyces cerevisiae YDR466w.
GN OrderedLocustNames=KLUA0503487g;
OS Kluyveromyces lactis (Yeast);
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
OX NCBI_TaxID=28985;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=CBS 2359 / IFO 1267 / NRRL Y-1140 / WM3;
RX PubMed=1529592; DOI=10.1038/nature02579;
RA Dujon B., Sherman D., Fischer G., Duret P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marck C., Neuvéglise C., Talla E.,
RA Goffard N., Frangeul L., Aigle M., Anthonard V., Babour A., Barbe V.,
RA Barney S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,
RA Boissarie A., Boyer J., Catolico L., Confalonieri F., de Darvar A.,
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
RA Hantreay F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA Niclaud J.-M., Nikolaki M., Ozias S., Ozler-Kalogeropoulos O.,
RA Pellenz S., Potier S., Richard G.-F., Straub M.-L., Suleau A.,
RA Swennen D., Tekala P., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA Zenlou-Meyer M., Zivanovic Y., Botocin-Fukunara M., Thierry A.,
RA Bouchier C., Caudron B., Scarpetti C., Galliard C., Weissbach J.,
RA Wincker P., Souciet J.-L.;
RT "Genome evolution in yeasts.";
RL Nature 430:35-44(2004).
CC -I- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
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CC -----
EMBL: CR382125; CAG99193.1; -; Genomic_DNA.
DR GO: GO:0005524; F:ATP binding; IEA.
DR GO: GO:0000156; F:nucleotide binding; IEA.
DR GO: GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO: GO:0016740; F:transferase activity; IEA.
DR GO: GO:0006468; P:autophagy; IEA.
DR GO: GO:0006468; P:protein amino acid phosphorylation; IEA.
DR GO: GO:0015031; P:protein transport; IEA.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR008271; Ser_thr_kin_A5.
DR InterPro: IPR002290; Ser_thr_kinase.
DR Pfam: PF00069; Pkinase; 1.
DR ProDom: PD000001; Prot_kinase; 1.
DR SMART: SM00220; S_TKc; 1.

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DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00011; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00108; PROTEIN KINASE_ST; 1.
KW ATP-binding; Complete proteome; Kinase; Nucleotide-binding;
KW Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 647 AA; 72882 MW; B11FA13D324B5DD9 CRC64;

Query Match 84.8%; Score 67; DB 2; Length 647;
Best Local Similarity 86.7%; Pred. No. 0.011;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 NSFVGTAGVSPPELL 16
Db 171 NSFVGTAGVSPPELL 185

RESULT 38
PKH1_YEAST STANDARD; PRT; 766 AA.
ID Q03407_YEAST
AC Q03407_YEAST
DT 31-AUG-2004, integrated into UniProtKB/Swiss-Prot.
DT 01-NOV-1996, sequence version 1.
DT 07-MAR-2006, entry version 40.
DE Serine/threonine-protein kinase PKH1 (EC 2.7.1.37) (3-
DE phosphoinositide-dependent protein kinase 1).
GN Name=PKH1, OrderedLocustNames=YDR490C;
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=S288c;
RX MEDLINE=97313263; PubMed=9169667;
RA Jacq C., Alt-Moerbe J., Andre B., Arnold W., Bahr A., Ballesca J.P.G.,
RA Barques M., Baron L., Becker A., Bileau N., Bloecher H., Bligeon C.,
RA Boskovic J., Brandt P., Brueckner M., Buhrago M.J., Cosser F.,
RA Delaveau T., del Rey F., Dujon B., Eide L.G., Garcia-Camalejo J.M.,
RA Goffeau A., Gomez-Peris A., Granotier C., Hanemann V., Hankeln T.,
RA Hohnle J.D., Jaeger W., Jimenez A., Joniaux J.-L., Kraemer C.,
RA Kuester H., Laamenen P., Legros Y., Louis E.J., Moeller-Rieker S.,
RA Monnet A., Moro M., Mueller-Auer S., Nussbaumer B., Particio N.,
RA Paulin L., Perea J., Perez-Alonso M., Perez-Ortin J.E., Pohl T.M.,
RA Prydz H., Purnelle B., Raamsen S.W., Remacha M.A., Revuelta J.L.,
RA Rieger M., Salom D., Saluz H.P., Salz U.E., Saren A.W., Schaefer M.,
RA Scharte M., Schmidt E.R., Schneider C., Scholler P., Schwarz S.,
RA Soler-Mira A., Urrutazu L.A., Verhaesselt P., Vissers S., Voet M.,
RA Volckaert G., Wagner G., Wambuit R., Wedler E., Wedler R., Woelfl S.,
RA Harris D.E., Bowman S., Brown D., Churcher C.M., Connor R., Dedman K.,
RA Gentles S., Hamlin N., Hunt S., Jones L., McDonald S., Murphy L.D.,
RA Niblett D., Odell C., Oliver K., Rajandream M.A., Richards C.,
RA Shore L., Walsh S.V., Barrett B.G., Dietrich F.S., Mulligan J.T.,
RA Allen E., Araujo R., Aviles E., Berno A., Carpenter J., Chen E.,
RA Cherry J.M., Chung E., Duncan M., Hunnicke-Smith S., Hyman R.W.,
RA Komp C., Lashkari D., Lew H., Lin D., Mosedale D., Nakahara K.,
RA Nannath A., Oelner P., Oh C., Patel F.X., Roberts D., Schramm S.,
RA Schroeder M., Shogren T., Shroff N., Wiant N., Yellon M.A.,
RA Boستein D., Davis R.W., Johnston M., Andrews S., Brinkman R.,
RA Cooper J., Ding H., Du Z., Favello A., Fulton L., Gattung S.,
RA Greco T., Hallsworth K., Hawkins J., Hillier L.W., Jier M.,
RA Johnson D., Johnston L., Kirsten J., Kucaba T., Langston Y.,
RA Lacroix P., Le T., Mardis E., Meneses S., Miller N., Nian M.,
RA Pauley A., Paluso D., Rifkin L., Riles L., Tach A., Trevaastis E.,
RA Vignat D., Wilcox L., Woldman P., Vaudin M., Wilson R.,
RA Waterson R., Albermann K., Hani J., Heumann K., Kleine K.,
RA Meues H.-W., Zollner A., Zaccaria P.;
RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome IV.";
RL Nature 387:75-78(1997).
RN [2]
RP FUNCTION.
RX MEDLINE=99175477; PubMed=10074427; DOI=10.1016/S0960-9822(99)80088-8;
RA Casamayor A., Torrance P.D., Kobayashi T., Thorner J., Alessi D.R.;
RA "Functional counterparts of mammalian protein kinases PDK1 and SGK in

```

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RT budding yeast."
RL Curr. Biol. 9:186-197(1999).
CC -1- FUNCTION: Activates YPK1 by phosphorylating of a threonine
CC residue.
CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -1- INTERACTION:
CC P32322:YOR086C; Nbdexp1; InactEBI-32467, EBI-23225;
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PDK1
CC subfamily.
CC -----
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CC -----
DR EMBL: U13050, AAB64917.1, -, Genomic_DNA.
DR PIR: S69657, S69657.
DR HSSP: O15530, IH1W.
DR IntAct: Q03407, -.
DR Ensembl: YDR490C, Saccharomyces cerevisiae.
DR GenomeReviews: Z71256_GR, YDR490C.
DR SGD: S000002898, PKH1.
DR Linkhub: Q03407, -.
DR GO: GO:0005829; C:cytosol, IDA.
DR GO: GO:0005515; F:protein binding, IPI.
DR GO: GO:0004672; F:protein kinase activity, IDA.
DR GO: GO:0006897; P:endocytosis, IMP.
DR GO: GO:0000196; P:MAPKK cascade during cell wall biogenesis, IGI.
DR GO: GO:0006468; P:protein amino acid phosphorylation, IDA.
DR InterPro: IPR000719, Prot_kinase.
DR InterPro: IPR008271, Ser_thr_pkin_AS.
DR InterPro: IPR002290, Ser_thr_pkinase.
DR InterPro: IPR001245, Tyr_pkinase.
DR Pfam: PF00069, Pkinase; 1.
DR ProDom: PD000001, Prot_kinase; 1.
DR SMART: SM00220, S_TKc; 1.
DR PROSITE: PS00107, PROTEIN KINASE ATP; 1.
DR PROSITE: PS50011, PROTEIN KINASE DOM; 1.
DR PROSITE: PS00108, PROTEIN KINASE ST; 1.
DR ATP-binding; Complete proteome; Kinase; Nucleotide-binding;
KW Serine/threonine-protein kinase; Transferase.
KM CHAIN 1 766
FT DOMAIN 125 391 /Prid=PRO_0000086552.
FT NP_BIND 131 139 ATP (By similarity).
FT ACT_SITE 249 249 Proton acceptor (By similarity).
FT BINDING 154 154 ATP (By similarity).
FT SEQUENCE 766 AA; 86253 MW; 7FDD2EB8B8C367 CRC64;

Query Match 84.8%; Score 67; DB 1; Length 766;
Best Local Similarity 81.2%; Pred. No. 0.013;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ANSFVGTAGYVSPPELL 16
DB 294 SKSFVGTAEYVSPPELL 309

RESULT 39
Q6FMN9_CANGA PRELIMINARY; PRT; 991 AA.
AC Q6FMN9;
DT 19-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 21-JUL-2004, sequence version 1.
DE 19-JUL-2004, entry version 22.
DE 21-FEB-2006, entry version 1.
DE 5-miRNAs with tr|Q03306 Saccharomyces cerevisiae YDR466w.
GN OrderedLocustNames=CAGLCK06479g;
OS Candida glabrata (Yeast) (Torulopsis glabrata).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX NCBI_TaxID=5478;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=ATCC 2001 / CBS 138;
RX PubMed=15229592; DOI=10.1038/nature02579;

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RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,
RA Goffard N., Frangeul L., Aigle M., Anhouard V., Babour A., Barbe V.,
RA Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,
RA Boismare A., Boyer J., Catolico L., Confanioli F., de Barvar A.,
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Gropi A.,
RA Hantreay F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
RA Kerret A., Kozul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA Nicand J.-M., Nikolski M., Ortas S., Orlat-Kalogoropoulos O.,
RA Pellenn S., Potier S., Richard G.-F., Strub M.-L., Suleau A.,
RA Swennen D., Tekla F., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA Zenilou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,
RA Boucher C., Caudron B., Scarpeilli C., Gallardin C., Weissenbach J.,
RA Wincker P., Souciet J.-L.;
RA "Genome evolution in yeasts.";
RT Nature 430:35-44(2004).
RL Nature 430:35-44(2004).
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
CC -----
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CC Distributed under the Creative Commons Attribution-NonDerivs License
CC -----
DR EMBL: CR380957, CAG61466.1, -, Genomic_DNA.
DR GO: GO:0005524; F:ATP binding, IEA.
DR GO: GO:0000166; F:nucleotide binding, IEA.
DR GO: GO:0004674; F:protein serine/threonine kinase activity, IEA.
DR GO: GO:0016740; F:transferase activity, IEA.
DR GO: GO:0006914; P:autophagy, IEA.
DR GO: GO:0006468; P:protein amino acid phosphorylation, IEA.
DR GO: GO:0015031; P:protein transport, IEA.
DR InterPro: IPR000719, Prot_kinase.
DR InterPro: IPR008271, Ser_thr_pkin_AS.
DR InterPro: IPR002290, Ser_thr_pkinase.
DR InterPro: IPR001245, Tyr_pkinase.
DR Pfam: PF00069, Pkinase; 1.
DR ProDom: PD000001, Prot_kinase; 1.
DR SMART: SM00220, S_TKc; 1.
DR PROSITE: PS00107, PROTEIN KINASE ATP; UNKNOWN_1.
DR PROSITE: PS50011, PROTEIN KINASE DOM; 1.
DR PROSITE: PS00108, PROTEIN KINASE ST; 1.
DR ATP-binding; Complete proteome; Kinase; Nucleotide-binding;
KW Serine/threonine-protein kinase; Transferase.
KM SEQUENCE 991 AA; 111045 MW; DE8A9434593A6CE CRC64;

Query Match 84.8%; Score 67; DB 2; Length 991;
Best Local Similarity 86.7%; Pred. No. 0.017;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 NSFVGTAGYVSPPELL 16
DB 195 SSFVGTAEYVSPPELL 209

RESULT 40
Q753H7_ASHGO PRELIMINARY; PRT; 1033 AA.
AC Q753H7;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 21-FEB-2006, entry version 22.
DE AFR335CP.
GN OrderedLocustNames=AFR335C;
OS Ashbya gossypii (Yeast) (Bremothecium gossypii).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Bremothecium.
OX NCBI_TaxID=33169;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=ATCC 10895;
RX PubMed=15001715; DOI=10.1126/science.1095781;
RA Dietrich F.S., Voegel S., Brachet S., Letch A., Gates K., Stetner S.,
RA Mohr C., Poehlmann R., Luedi P., Choi S., Wing R.A., Flavler A.,
RA Gaffney T.D., Philippen P.;
RA "The Ashbya gossypii genome as a tool for mapping the ancient

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RT Saccharomyces cerevisiae genome."
RL Science 304:304-307(2004).
CC -I- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
CC -----
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CC -----
CC EMBL: AE016819; AAS53706.1; -; Genomic_DNA.
DR HSSP; P05132; 1ATP.
DR AGD; AFR353C; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0000166; F:nucleotide binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006914; P:autophagy; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR GO; GO:0015031; P:protein transport; IEA.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR008271; Ser_Thr_kin_AS.
DR InterPro; IPR002290; Ser_Thr_kinase.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Complete proteome; Kinase; Nucleotide-binding;
KW Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 1033 AA; 114371 MW; B284CD848CE38B CRC64;

Query Match 84.8%; Score 67; DB 2; Length 1033;
Best Local Similarity 81.2%; Pred. No. 0.018;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ANSFVGTAGVYSPELL 16
Db 366 SKSFVGTAEVYSPELL 381

RESULT 41
ID 06FOB9_CANGA PRELIMINARY; PRT; 1076 AA.
AC 06FOB9;
DT 19-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 19-JUL-2004, sequence version 1.
DT 21-FEB-2006, entry version 22.
DE Similar to sp|Q12236 Saccharomyces cerevisiae YOL100w PKH2.
GN OrderedLocusNames=CAGL0107513g;
OS Candida glabrata (Yeast) (Torulopsis glabrata).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX NCBI_TaxID=5478;

RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=ATCC 2001 / CBS 138;
RX PubMed=15229592; DOI=10.1038/nature02579;
RA Lafontaine I., de Montigny J., Marck C., Neveglie C., Talla E.,
RA Goffard N., Frangeul L., Aigle M., Anichoud V., Babbour A., Barde V.,
RA Batnany S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,
RA Boissarie A., Boyer J., Catolico L., Confantolero F., de Daruvar A.,
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
RA Hantave F., Henequin C., Jauniaux N., Joyet P., Kachouri R.,
RA Kerrest A., Koszul R., Lemaire M., Leaur I., Ma L., Muller H.,
RA Nicaud J.-M., Nikolaki M., Oztas S., Ozler-Kalogeropoulos O.,
RA Pelland S., Potier S., Richard G.-F., Straub M.-L., Suleau A.,
RA Swennen D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA Zenou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,
RA Bouchier C., Caudron B., Scarpelli C., Galliard C., Weissenbach J.,
RA Wincker P., Souciet J.-L.,
RT "Genome evolution in yeasts."
RL Nature 430:35-44(2004).

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CC -I- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
CC -----
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CC -----
CC EMBL: CR380955; CAG60512.1; -; Genomic_DNA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0000166; F:nucleotide binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006914; P:autophagy; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR GO; GO:0015031; P:protein transport; IEA.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR008271; Ser_Thr_kin_AS.
DR InterPro; IPR002290; Ser_Thr_kinase.
DR InterPro; IPR01245; Tyr_kinase.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Complete proteome; Kinase; Nucleotide-binding;
KW Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 1076 AA; 120986 MW; C52DAD0AF34EEAFD CRC64;

Query Match 84.8%; Score 67; DB 2; Length 1076;
Best Local Similarity 81.2%; Pred. No. 0.019;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ANSFVGTAGVYSPELL 16
Db 349 SKSFVGTAEVYSPELL 364

RESULT 42
ID KOKO_YEAST STANDARD; PRT; 1081 AA.
AC Q12236;
DT 01-NOV-1997, integrated into UniProtKB/Swiss-Prot.
DT 01-NOV-1996, sequence version 1.
DT 07-MAR-2006, entry version 45.
DE Probable serine/threonine-protein kinase YOL100W (EC 2.7.1.37).
GN OrderedLocusNames=YOL100W; ORFNames=HRC1081;
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;

RN NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RP MEDLINE=9607631; PubMed=7502582;
RX Vandenbol M., Durand P., Portetelle D., Hilger F.,
RA Vandenbol M., Durand P., Portetelle D., Hilger F.,
RT "Sequence analysis of a 44 kb DNA fragment of yeast chromosome XV
RT including the TY1-H3 retrotransposon, the sufl(+) frameshift
RT suppressor gene for tRNA-Gly, the yeast transfer RNA-Thr1a and a
RT delta element."
RL Yeast 11:1069-1075(1995).

RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=S288c / FY1679;
RX MEDLINE=97313270; PubMed=9169874;
RA Dujon B., Albermann K., Aldea M., Alexandraki D., Ansoorge W.,
RA Arino J., Benes V., Bohn C., Bolotin-Fukuhara M., Bordonne R.,
RA Boyer J., Camasse A., Casamayor A., Cazaes C., Charet G.,
RA Czegluch C., Daignan-Fornier B., Dang V.-D., de Haan M., Delius H.,
RA Durand P., Fairhead C., Feldmann H., Gallion L., Galleeson F.,
RA Gano F.-J., Gancedo C., Goffeau A., Goulding S.E., Grivell L.A.,
RA Habbig B., Hand N.J., Han J., Hattenhocht U., Hebling U.,
RA Hernandez Y., Herrero E., Heumann K., Hiesel R., Hilger F., Hofmann B.,
RA Hollenberg C.P., Hughes B., Jauniaux J.-C., Kalogeropoulos A.,
RA Katsoulou C., Koides E., Lafontaine M.J., Landt O., Louis E.J.,
RA Maarse A.C., Madania A., Mannhaupt G., Marck C., Martin R.P.,

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RA Mewes H.-W., Michaux G., Paces V., Parle-McDermott A.G., Pearson B.M.,
 RA Perrin A., Petersson B., Poch O., Pohl T.M., Poitey R.,
 RA Portetelle D., Pujol A., Purnelle B., Ramezani Rad M., Reckmann S.,
 RA Schwager C., Schweizer M., Sor F., Sterky F., Tarasov I.A.,
 RA Teodoru C., Tettein H., Thierly A., Tobiasch E., Tzeremla M.,
 RA Uhlen M., Unelid M., Valens M., Vandenbol M., Vetter I., Vilek C.,
 RA Voet M., Volckaert G., Voss H., Wambolt R., Wedler H., Wiemann S.,
 RA Wambolt R., Wolfe K.H., Zollner A., Zumbstein E., Kleine K.,
 RA "The nucleotide sequence of Saccharomyces cerevisiae chromosome XV.",
 RT Nature 387:98-102(1997).
 CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PKC
 CC subfamily.
 CC -----
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 CC -----
 CC EMBL: Z48149; CAAB8162.1; -; Genomic DNA.
 DR EMBL: Z74842; CAAG9113.1; -; Genomic DNA.
 DR PIR: S51899; S51899.
 DR HSP: O15530; 1HMW.
 DR IntAct: Q12236; -.
 DR GeneDB: Q12236; -.
 DR Ensembl: Y0L10W; Saccharomyces cerevisiae.
 DR GenomeReviews: Y13140 GR; Y0L10W.
 DR SGD: S000005460; PKH2_2.
 DR BioCyc: SCER-S28-01:SCER-S28-01-005381-MONOMER; -.
 DR LinkHub: Q12236; -.
 DR GO: GO:0005634; C:nucleus; IDA.
 DR GO: GO:0004672; F:protein kinase activity; IDA.
 DR GO: GO:0000196; P:MAPKK cascade during cell wall biogenesis; IGI.
 DR GO: GO:0006468; P:protein amino acid phosphorylation; IDA.
 DR InterPro: IPR000719; Prot_kinase.
 DR InterPro: IPR008271; Ser_thr_kin AS.
 DR InterPro: IPR002290; Ser_thr_kinase.
 DR InterPro: IPR001245; Tyr_kinase.
 DR Pfam: PF00069; Pkinase; 1.
 DR ProDom: PD000001; Prot_kinase; 1.
 DR SMART: SM00220; S_TKc; 1.
 DR PROSITE: PS00107; PROTEIN KINASE ATP 1.
 DR PROSITE: PS50011; PROTEIN KINASE DOM 1.
 DR PROSITE: PS00108; PROTEIN KINASE ST 1.
 KW ATP-binding; Complete proteome; Hypothetical protein; Kinase;
 KW Nucleotide-binding; Serine/threonine-protein kinase; Transferrase.
 FT CHAIN 1 1081 Probable serine/threonine-protein kinase
 FT Y0L10W.
 FT DOMAIN 179 443 /FtId=PRO_0000086158.
 FT NP_BIND 185 193 Protein kinase.
 FT ACT_SITE 303 303 ATP (By similarity).
 FT BINDING 208 208 Proton acceptor (By similarity).
 FT BINDING 1081 AA; 121660 MW; BE0DD9D949AC2BEC3 CRC64;
 SQ
 Query March 84.8%; Score 67; DB 1; Length 1081;
 Best Local Similarity 81.2%; Pred. No. 0.019; Indels 0; Gaps 0;
 Matches 13; Conservative 2; Mismatches 1;
 Oy 1 ANSFGTAQVYSPELL 16
 Db 346 SKSFVGTAEVYSPELL 361
 RESULT 43
 PDFT1 DROME
 ID GPMK1 DROME STANDARD; PRT; 836 AA.
 AC 09M0V1; 062534; 053XF5; 07KVE1; 08HGG6; 09M0V2; 09M0V3;
 DT 16-OCF-2001; Integrated into UniProtKB/Swiss-Prot.
 DT 24-JAN-2006; Sequence version 4.
 DT 07-MAR-2006; entry version 45.
 DE 3-phosphoinositide-dependent protein kinase 1 (EC 2.7.1.37) (dPK-1)
 DE (serine/threonine-protein kinase 61C) (dSTPK61).
 GN Name=PK61C; Synonyms=PK1; ORFNames=CG1210;
 OS Drosophila melanogaster (fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 CX NCBI_TaxID=7227;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 2), AND FUNCTION.
 RX PubMed=10336630;
 RA PubMed=10336630;
 RT "Sex-specific transcripts of the dPck1 serine/threonine kinase gene
 in Drosophila melanogaster.";
 RL Eur. J. Biochem. 262:456-466(1999).
 RN [2]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=Berkley;
 RX MEDLINE=20196006; PubMed=10731132; DOI=10.1106/science.287.5461.2185;
 RA Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Morten J.R., Vandeil M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazek R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-O., Andrews-Plambeck C., Baldwin D.,
 RA Ballwe R.M., Baas A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Casley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablo B., Delcher A., Deng Z., Maye A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doug L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Dublin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foeller C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Idegawa C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Krevitz S., Kulp D., Lai Z.,
 RA Lanko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
 RA Liu X., Matrei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy J., Muzny D.M., Nelson D.L.,
 RA Nelson S.M., Nelson K.A., Nixon K., Nuskehn D.R., Pacleb J.M.,
 RA Palazolo M., Peltman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun B.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weisenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195(2000).
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 RP GENOME REANNOTATION, AND ALTERNATIVE SPLICING.
 RX MEDLINE=22426069; PubMed=12537572;
 RA Miera S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk S.E.,
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
 RA Bertencourt B.R., Celisner S.E., de Grey A.D.N.J., Drysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schneider A.J., Shu S.Q.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.B.;
 RT "Annotation of the Drosophila melanogaster euchromatic genome: a
 systematic review.";
 RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
 RN [4]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORMS 1, 2 AND 3).
 RC STRAIN=Berkley; TISSUE=Embryo, and Testis;
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.M.,
 RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Fritze E.,
 RA George R.A., Gonzalez M., Guarin H., Krommiller B., Li P.W., Liao G.,
 RA Miranda A., Mungall C.J., Nunoo J., Pacleb J.M., Paragas V., Park S.,

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